

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 17:33:48 ; Search time 8749 Seconds
(without alignments)
11043.514 Million cell updates/sec

Title: US-09-377-795-1
Perfect score: 1994
Sequence: 1 ggcacgagcatggcccttgt.....gtaaaaaaaaaaaaaaaaa 1994

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_bcs:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1848.4	92.7	1990	9	BC050612	BC050612 Homo sapi
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7	1836.4	92.1	2121	9	AF261086	AF261086 Homo sapi
8	1832.6	91.9	1975	9	AF062089	AF062089 Homo sapi
9	1823	91.4	2009	6	BD135431	BD135431 Receptor
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11	1823	91.4	2009	6	AR534835	AR534835 Sequence
12	1823	91.4	2009	6	AX017214	AX017214 Sequence
13	1757.2	88.1	2034	6	BD135432	BD135432 Receptor
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18	1235.4	62.0	1666	9	AK000593	AK000593 Homo sapi
19	1021.6	51.2	2175	4	BTA414557	BJ414557 Bos tauru

20	945.6	47.4	1798	10	AF513109	AF513109 Mus muscu
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25	902.4	45.3	1239	10	AY392762	AY392762 Rattus no
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ALIGNMENTS

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DEFINITION
AF074382
VERSION AF074382.1 GI:3641279
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1994)
AUTHORS Rothwarf,D.M., Zandi,E., Natoli,G. and Karin,M.
TITLE IKK-gamma is an essential regulatory subunit of the IkbapB kinase complex
JOURNAL Nature 395 (5699), 297-300 (1998)
MEDLINE 98421680
PUBMED 9751060
REFERENCE 2 (bases 1 to 1994)
AUTHORS Rothwarf,D.M., Zandi,E., Natoli,G. and Karin,M.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1998) Pharmacology, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0636, USA

AF074382 Homo sapiens Ikb kinase gamma subunit (IKK-gamma) mRNA, complete
AF074382.1 GI:3641279
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Rothwarf,D.M., Zandi,E., Natoli,G. and Karin,M.
IKK-gamma is an essential regulatory subunit of the IkbapB kinase complex
Nature 395 (5699), 297-300 (1998)
98421680
9751060
2 (bases 1 to 1994)
Rothwarf,D.M., Zandi,E., Natoli,G. and Karin,M.
Direct Submission
Submitted (25-JUN-1998) Pharmacology, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0636, USA

→ 9/98

FEATURES
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ORIGIN

Query Match	100.0%	Score 1994;	DB 9;	Length 1994;
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DB 121	GAGTCCCATCAGCCCTTGGCCCTGTGTGATGAATAGGACCTCTGGAAGAGCCAACTGTG	180		
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RESULT 2
BC012114
LOCUS
DEFINITION
Homo sapiens inhibitor of kappa light polypeptide gene enhancer in
B-cells, kinase-gamma, mRNA (cDNA clone MGC:20127 IMAGE:4651870),
complete cds.
ACCESSION
BC012114
VERSION
BC012114.1 GI:15082398
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2071)
AUTHORS
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalls, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2071)
Strausberg, R.
Direct Submission
Submitted (02-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgi.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywicki, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Fawan Pandoh, Anna-Lisa Prabhu, Farvaneh Saeedi, Jacqueline
Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 29 Row: 0 Column: 12
This clone was selected for full length sequencing because it
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DB 14 CAGGCCATGGCCCTTGTGATCCAGTGGGGAAACTAAGGCCAGAGAAGTCAGGACCCC 73
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ORIGIN

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QY	238	GTCTCTCTGGGGAAGCCAGCATGTCACCTGCTTCCAGAACAGGGCGCTCTTGAGAC	297		
DB	314	GTCTCTCTGGGGAAGCCAGCATGTCACCTGCTTCCAGAACAGGGCGCTCTTGAGAC	373		
QY	298	CTCCAGCGCTGCTGGAGAGAACTCAAGAGCTCCGAGATGCCATCCGCGCAGACCA	357		
DB	374	CCTCCAGCGCTGCTGGAGAGAACTCAAGAGCTCCGAGATGCCATCCGCGCAGACCA	433		
QY	358	GATTTCCGGGAGCGCTGGAGAGCTCTGCATTTCCAAAGCCAGCCAGAGGAGGAGAA	417		
DB	434	GATTTCCGGGAGCGCTGGAGAGCTCTGCATTTCCAAAGCCAGCCAGAGGAGGAGAA	493		
QY	418	GGAGTTCTCATGTGCAAGTTCCAGGAGCCAGGAACTGGTGGAGAGACTCGGCTTGA	477		
DB	494	GGAGTTCTCATGTGCAAGTTCCAGGAGCCAGGAACTGGTGGAGAGACTCGGCTTGA	553		
QY	478	GAACTCGATCTGAAGAGCAGAGAGCAGAGCTCTCGGGAGGTGGAGCACTGAAGAG	537		
DB	554	GAACTCGATCTGAAGAGCAGAGAGCAGAGCTCTCGGGAGGTGGAGCACTGAAGAG	613		
QY	538	ATGCCAGCAGCAGATGGCTGAGGACAAAGCCCTCTGTGAAGCCAGGTGACCTCTTGCT	597		
DB	614	ATGCCAGCAGCAGATGGCTGAGGACAAAGCCCTCTGTGAAGCCAGGTGACCTCTTGCT	673		
QY	598	CGGGAGCTGACGAGAGCAGAGTCCGCTTGAGGCTGCGCACTAAGGAATGCCAGCTCT	657		
DB	674	CGGGAGCTGACGAGAGCAGAGTCCGCTTGAGGCTGCGCACTAAGGAATGCCAGCTCT	733		
QY	658	GGAGGGTCCGGGCCCGGCGCAGCAGAGCAGCGCGGCGAGCTGGAGAGTGAAGCGGAGGC	717		
DB	734	GGAGGGTCCGGGCCCGGCGCAGCAGAGCAGCGCGGCGAGCTGGAGAGTGAAGCGGAGGC	793		
QY	718	GCTGACAGCAGCAGCAGAGTGCAGTGCAGCTGCGCATGCCAGGGCCAGAGCGTGA	777		
DB	794	GCTGACAGCAGCAGCAGAGTGCAGTGCAGCTGCGCATGCCAGGGCCAGAGCGTGA	853		
QY	778	GGCCCGCTCCGATGAGCGCCAGCCCTCGGAGGAGAGAGAGTGGCCAGTT	837		
DB	854	GGCCCGCTCCGATGAGCGCCAGCCCTCGGAGGAGAGAGAGTGGCCAGTT	913		
QY	838	GCAGTGGCTTATCAACAGCTCTTCCAGAACTACAGCAACCAATCAAGAGCAGCGTGT	897		
DB	914	GCAGTGGCTTATCAACAGCTCTTCCAGAACTACAGCAACCAATCAAGAGCAGCGTGT	973		

QY	898	GGGAGTGCAGCGAAGCGAGGAATCAGCTGGAAAGATCTCAAAAGCAGCAGCTCCAGCAGC	957
DB	974	GGGAGTGCAGCGAAGCGAGGAATCAGCTGGAAAGATCTCAAAAGCAGCAGCTCCAGCAGC	1033
QY	958	CGAGAGCCCTGTTGGCCAAACAGAGGTGATCGATGAAGCTGAAGGAGGAGCGGAGCA	1017
DB	1034	CGAGAGCCCTGTTGGCCAAACAGAGGTGATCGATGAAGCTGAAGGAGGAGCGGAGCA	1093
QY	1018	GCACAAGATTGTGATGGAGACCGTTCCGTTGCTGAAGCCCGGAGGATATCTACAAGC	1077
DB	1094	GCACAAGATTGTGATGGAGACCGTTCCGTTGCTGAAGCCCGGAGGATATCTACAAGC	1153
QY	1078	GGACTTCCAGGCTGAGAGCGAGGCCCGGAGAAAGCTGGCCGAGAGAAAGAGTCTCTGCA	1137
DB	1154	GGACTTCCAGGCTGAGAGCGAGGCCCGGAGAAAGCTGGCCGAGAGAAAGAGTCTCTGCA	1213
QY	1138	GGAGCAGCTGGAGCAGCTGCGAGAGGAGTACAGCAAACTGAAGGCCAGCTGTCAAGAGTC	1197
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DB	1274	GGCAGAGATCGAGGACATGAGGAAGCGGATGTGAGGTCTCCAGGCCCTTGGCCCC	1333
QY	1258	CGCCCCCTGCTACCTCTCTCTCCCTGGCCCTGCGCAGCAGAGAGGAGGCCCCCGA	1317
DB	1334	CGCCCCCTGCTACCTCTCTCTCCCTGGCCCTGCGCAGCAGAGAGGAGGCCCCCGA	1393
QY	1318	GGAGCCACTGACTTCTGCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCT	1377
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QY	1438	CGAGAGCTGTCGCGGAGCCGTCGAGTCTGCGCTTCTCTCCGCTGCTGCTAGCCAGGA	1497
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DB	1573	TGAAGGCTGGGTGGCCCAAACTGGGATGCCACTGGAGGCCCAACCCAGGAGCTGGCCGC	1632
QY	1558	GGCACTTACGCTTACGCTGTTGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1617
DB	1633	GGCACTTACGCTTACGCTGTTGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1692
QY	1618	GATCAGGCTGACTGCTGCTCTTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1677
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QY	1678	GGCTAATCCCTCCCTCTTCTCCACCCGCGCATGCGGGAAGTCAAGAAATGGGGCTGGGGC	1737
DB	1753	GGCTAATCCCTCCCTCTTCTCCACCCGCGCATGCGGGAAGTCAAGAAATGGGGCTGGGGC	1812
QY	1738	TCTCAGGAGAACTGCTTCCCTGCGCAGAGCTGGGGTGGAGCTCTTCTCCCAACCGGACA	1797
DB	1813	TCTCAGGAGAACTGCTTCCCTGCGCAGAGCTGGGGTGGAGCTCTTCTCCCAACCGGACA	1872
QY	1798	CCGACCCCGCCGCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1857
DB	1873	CCGACCCCGCCGCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1932
QY	1858	TCCTTTTGGGCTGCTATGCTATTTCCATTTTGCACGAGCCGATGTGTATTTTAAACAGTCA	1917
DB	1933	TCCTTTTGGGCTGCTATGCTATTTCCATTTTGCACGAGCCGATGTGTATTTTAAACAGTCA	1992
QY	1918	CTATTGATGGACATTTGGGTTGTTTCCCATCTTTTGTGTTTACCATAAATATGGCATAGTA	1977
DB	1993	CTATTGATGGACATTTGGGTTGTTTCCCATCTTTTGTGTTTACCATAAATATGGCATAGTA	2052

QY 1978 AAAA 1981
 Db 2053 AAAA 2056

RESULT 4
 BC000299
 LOCUS
 DEFINITION Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma, mRNA (CDNA clone MGC:8374 IMAGE:2820134), complete cds.

ACCESSION BC000299
 VERSION BC000299.2 GI:33875269
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1966)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huly, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1966)
 AUTHORS Strausberg, R.L.
 TITLE Direct Submission
 JOURNAL Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK COMMENT
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 19, 2003 this sequence version replaced gi:12653066.
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgrl.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgoun, C., Voet, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 1 Row: c Column: 5

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361093.

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 /notes="Smc; Region: Chromosome segregation ATPases [Cell division and chromosome partitioning]"
 /db_xref="CDD:COG1196"

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 Db 103 CAGCCCTTCCTCCCTGTTGGATGATAGGACCTCTGGAAGAGCCAACTGTGTGAGATGGTG 162
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 Db 163 CAGCCAGTGTGTGGCCCGGCAGCAGATCAGGACGTAAGGCGAAGAGTCTCTCTGGGG 222
 QY 251 AAGCCAGCATGCTGCACCTGCTTTCAGAACAGGGCGCTCTTGAGACCTTCCAGCGCTGC 310
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 Db 283 CTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGCAGAGCAACAGAGTCTCTGGGG 342
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 QY 491 AAGAGCCAGAGGAGCAGGCTCTCGGCGAGGTGGAGCACTTCAAGAGATGCCAGAGCAGCAG 550
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Qy 1511 GGCACAACCTGGATGCGACCTGGAGGCGCCACCCAGAGAGCTGCGCGGACCTTACGCT 1570
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Qy 1991 AAAA 1994
Db 1962 AAAA 1965

RESULT 5
BC050612 1990 bp mRNA linear PRI 07-OCT-2003
LOCUS Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma, mRNA (cDNA clone MGC:60070 IMAGE:6062527), complete cds.
DEFINITION BC050612
ACCESSION BC050612.2 GI:34193533
VERSION BC050612.2
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1990)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butler, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1990)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT On Aug 25, 2003 this sequence version replaced gi:29792041.

FEATURES		Location/Qualifiers	
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	QY	1571	TCAGCTGTTGATCCGCTGCTGCTCTTTTGGGATAGATGGGCCCCGATAGGCGCTGAC
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DEFINITION AF091453			
VERSION AF091453.1 GI:5031140			
KEYWORDS			
SOURCE Homo sapiens (human)			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
Jin,D.Y., and Jeang,K.T.			
Isolation of full-length cDNA and chromosomal localization of human NF-kappaB modulator NEMO to Xq28			
J. Biomed. Sci. 6 (2), 115-120 (1999)			
JOURNAL			
MEDLINE 99189402			
PUBMED 10087442			
REFERENCE			
Jin,D.Y., Giordano,V., Kibler,K.V., Nakano,H. and Jeang,K.T.			
Role of adapter function in oncoprotein-mediated activation of NF-kappaB. Human T-cell leukemia virus type I tax interacts directly with IkappaB kinase gamma			
J. Biol. Chem. 274 (25), 17402-17405 (1999)			
JOURNAL			
MEDLINE 99292691			
PUBMED 10364167			
REFERENCE			
Jin,D.Y.			
Direct Submission			
Submitted (13-SEP-1998) LMM, NIAID/NIH, 9000 Rockville Pike, Bethesda, MD 20892-0460, USA			
JOURNAL			
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Db	229	AGCCAGTGTGGTGGCCGCGCAGATCAGAGCTACTGGGCGAAGAGTCTCTCTGGGGA	288
QY	252	AGCCAGCATGCTGCACCTGCTTCAGAACAGGGCGCTCTGAGACCTCCAGCGCTGCC	311
Db	289	AGCCAGCATGCTGCACCTGCTTCAGAACAGGGCGCTCTGAGACCTCCAGCGCTGCC	348
QY	312	TGGAGGAGAACTCAAGAGCTCCGAGATGCCATCCGCGAGACCAACAGATTTCTGCGGGAGC	371
Db	349	TGGAGGAGAACTCAAGAGCTCCGAGATGCCATCCGCGAGACCAACAGATTTCTGCGGGAGC	408
QY	372	GCTGCGAGAGCTTCTGCATTTTCAAGCCAGCAGAGGAGGAGAGGATTTCTCATGT	431
Db	409	GCTGCGAGAGCTTCTGCATTTTCAAGCCAGCAGAGGAGGAGAGGATTTCTCATGT	468
QY	432	GCNAGTTCAGAGGCGCCAGGAAACTGTGTGGAGAGACTCGGCTGAGAGCTCGATCTCA	491
Db	469	GCNAGTTCAGAGGCGCCAGGAAACTGTGTGGAGAGACTCGGCTGAGAGCTCGATCTCA	528
QY	492	AGAGCAGAGGAGCAGAGCTCTGCGGGAGGTGGAGCACTGAAGAGATGCCAGCAGCAGA	551
Db	529	AGAGCAGAGGAGCAGAGCTCTGCGGGAGGTGGAGCACTGAAGAGATGCCAGCAGCAGA	588
QY	552	TGGCTGAGGACAAAGCCCTCTGTGAAAGCCAGGTGACGCTCTTGTCTCGGGAGTGCAGG	611
Db	589	TGGCTGAGGACAAAGCCCTCTGTGAAAGCCAGGTGACGCTCTTGTCTCGGGAGTGCAGG	648
QY	612	AGAGCCAGAGTCTGAGAGCTGCACCTAGGAATGCCAGGCTCTGGAGGCTCCGGCCC	671
Db	649	AGAGCCAGAGTCTGAGAGCTGCACCTAGGAATGCCAGGCTCTGGAGGCTCCGGCCC	708
QY	672	GGGCGGCCAGCAGCAGCGCGGCGAGCTGGAGAGTGAGCGCGCGCTTGCAGCAGCAGC	731
Db	709	GGGCGGCCAGCAGCAGCGCGGCGAGCTGGAGAGTGAGCGCGCGCTTGCAGCAGCAGC	768
QY	732	ACAGCGTCAGGTGACAGCTGCGCATGCGAGGCGCAGAGCGTGGAGGCGCGCTCCGCA	791
Db	769	ACAGCGTCAGGTGACAGCTGCGCATGCGAGGCGCAGAGCGTGGAGGCGCGCTCCGCA	828

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ORIGIN

Query Match 91.9%; Score 1832.6; DB 9; Length 1975;
 Best Local Similarity 99.7%; Pred. No. 3e-298;
 Matches 1846; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 131 CAGCCCTTGCCTGTGGATGAATAGGCACCTCTGGAGAGCCAACTGTGTGAGATGGTG 190
 DB 93 CAGCCCTTGCCTGTGGATGAATAGGCACCTCTGGAGAGCCAACTGTGTGAGATGGTG 152

QY 191 CAGCCAGTGGTGGCCGCGCAGCATCAGACGTACTGGCGGAAGAGTCTCTCTGGGG 250
 DB 153 CAGCCAGTGGTGGCCGCGCAGCATCAGACGTACTGGCGGAAGAGTCTCTCTGGGG 212

QY 251 AAGCCAGCATGCTGCACCTGCTTCAGAACAGGGCGCTCTGAGACCCCTCCAGCGCTGC 310
 DB 213 AAGCCAGCATGCTGCACCTGCTTCAGAACAGGGCGCTCTGAGACCCCTCCAGCGCTGC 272

QY 311 CTGGAGGAGATCAAGAGCTCCGAGATCCATCCGCGCAGAGCAACCCAGATTTCTCGGGAG 370
 DB 273 CTGGAGGAGATCAAGAGCTCCGAGATCCATCCGCGCAGAGCAACCCAGATTTCTCGGGAG 332

QY 371 CGCTCGGAGGACTTCTGCATTTCCAGCCAGCCAGAGGAGGAGAGAGTTCCTCATG 430
 DB 333 CGCTCGGAGGACTTCTGCATTTCCAGCCAGCCAGAGGAGGAGAGAGTTCCTCATG 392

QY 431 TGCAGATTTCCAGGAGGCGCAGGAACTCGTGGAGAGACTCGGCCCTGGAGAGCTCGATCTG 490
 DB 393 TGCAGATTTCCAGGAGGCGCAGGAACTCGTGGAGAGACTCGGCCCTGGAGAGCTCGATCTG 452

QY 491 AAGAGCGAAGAGAGCAGGCTCTCGGAGTGGAGCACTTGAAGAGATGCCAGCAGCAG 550
 DB 453 AAGAGCGAAGAGAGCAGGCTCTCGGAGTGGAGCACTTGAAGAGATGCCAGCAGCAG 512

QY 551 ATGGCTGAGGCAAGGCTCTGTGAAGCCAGGTGACGTCTTCTCGGGGAGCTGCAG 610
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QY 611 GAGAGCCAGAGTCGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGGTCTGGGCC 670
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QY 671 CGGGCGGCAGCAGCAGCGCGGAGCTGGAGAGTGGAGCGCAGGCGCTGCAGCAGCAG 730
 DB 633 CGGGCGGCAGCAGCAGCGCGGAGCTGGAGAGTGGAGCGCAGGCGCTGCAGCAGCAG 692

QY 731 CACAGCGTGCAAGTGGACCTGGCATGSCAGGCCAGAGCGTGGAGGCGCGGCTCCGC 790
 DB 693 CACAGCGTGCAAGTGGACCTGGCATGSCAGGCCAGAGCGTGGAGGCGCGGCTCCGC 752

QY 791 ATGGAGCGCCAGGCGCCTCGGAGGAGAAAGAGTGGCCCAAGTTGCCAGGTGGCGCTAT 850
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QY 851 CACCAGCTCTTCCAAAGAAATACAGAACCAATCAAGAGCAGCGTGGTGGCAGTGAAGCGG 910
 DB 813 CACCAGCTCTTCCAAAGAAATACAGAACCAATCAAGAGCAGCGTGGTGGCAGTGAAGCGG 872

QY 911 AAGCCAGGAGATGCAGCTGGAAGATCTCAACAGCAGCTCCAGCAGGCGCGAGGAGGCCCTG 970
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RESULT 9
 BD135431
 LOCUS
 DEFINITION

BD135431 2009 bp DNA linear PAT 18-SEP-2002
 Receptor function regulator for TNF/NGF receptor family and other

QY 971 GTGCCAAACAGGAGGTGATCGATAAGCTGAAGGAGGAGCGGACGACACAAAGATTGTG 1030
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QY 1031 ATGGAGACCGTTCCGGTGTGAAGGCCGAGCGGATATCTACAAGGCCGACTTCCAGGCT 1090
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QY 1151 CAGCTGCAGAGGAGGTACACAACTCAAGGCCAGCTGTGAGGAGTCGGCCAGGATCGAG 1210
 DB 1113 CAGCTGCAGAGGAGGTACACAACTCAAGGCCAGCTGTGAGGAGTCGGCCAGGATCGAG 1172

QY 1211 GACATGAGGAAGCGGATGTGAGAGTCTCCAGGCCCTTTCGCCCCCGCCCTGCTCCCTAC 1270
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QY 1271 CTCTCTCTCCCTGGCCCTGCCAGCCAGAGGAGGCCCGCCGAGGAGCCAGCTGCAC 1330
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QY 1331 TTCTGTCTGCCCAAGTSCCAGTATCAGGCCCTCTGATATGGACACCTTCGACATATCATGTC 1390
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QY 1391 ATGGAGTGCATTCAGTAGGGCCCGCCAGTGCAGGCCACTGCTTGCCTGCCGAGGAGCTGCC 1450
 DB 1353 ATGGAGTGCATTCAGTAGGGCCCGCCAGTGCAGGCCACTGCTTGCCTGCCGAGGAGCTGCC 1411

QY 1451 GGGACGCTGAGTCTGGCGTTTCTCTCCGCGCTGCTAGCCAGGATGAAGGGCTGGGT 1510
 DB 1412 GGGACGCTGAGTCTGGCGTTTCTCTCCGCGCTGCTAGCCAGGATGAAGGGCTGGGT 1471

QY 1511 GGGCAACTGGGATGCCACTGGAGCCCAACCCAGAGCTGGCGCGGACACTTACGCT 1570
 DB 1472 GGGCAACTGGGATGCCACTGGAGCCCAACCCAGAGCTGGCGCGGACACTTACGCT 1531

QY 1571 TCAGCTGTGATCCGCTGGTCCCCTCTTTTGGGTAGATGGCGCCCGATCAGGCGCTGCAC 1630
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QY 1631 TCGCTGCTCTTTTGTTCCTCTGCTGCTGCAGACCACTTGCCTGGGCTAAATCCCTCC 1690
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QY 1691 CTCTTCTCCACCCGCGCACTGGGGAAGTCAAGAAATGGGGCTCTGGGGCTCTCAGGGAGAAC 1750
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QY 1751 TGCTTCCCTGGCAGAGCTGGGTGGAGCTCTTCTCCCAACCGGACACCGCCCGCCG 1810
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QY 1811 CGCTGTGCTGGAGTGGTGGCTCTTACCATGACACGGGTCTCTCTTTTGGGCTG 1870
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QY 1871 CATGCTATTCCATTTTTCAGCCAGACCGATGTGTATTTAAACCACTACTATTGATGGACA 1930
 DB 1832 CATGCTATTCCATTTTTCAGCCAGACCGATGTGTATTTAAACCACTACTATTGATGGACA 1891

QY 1931 TTTGGGTGTTCCTCCATCTTTTGTACCAATAAATATGGCATAGTAAAAA 1981
 DB 1892 TTTGGGTGTTCCTCCATCTTTTGTACCAATAAATATGGCATAGTAAAAA 1942

ACCESSION	BD135431	protein.	QY	611	GAGGCCAGAGTCGCTTGGAGGCTCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGGCC	670
VERSION	BD135431.1	GI:23230376	Db	616	GAGGCCAGAGTCGCTTGGAGGCTCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGGCC	675
KEYWORDS	JP 2002506644-A/1.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 2009)					
AUTHORS	Wallach,D., Kovalenko,A., Horwitz,M.S. and Li,Y.					
TITLE	Receptor function regulator for TNF/NGF receptor family and other proteins					
JOURNAL	Patent: JP 2002506644-A 1 05-MAR-2002; YEDA RESEARCH AND DEVELOPMENT CO LTD, ALBERT EINSTEIN COLLEGE OF MEDICINE					
COMMENT	OS Homo sapiens (human) PN JP 2002506644-A/1 PD 05-MAR-2002 PR 18-MAR-1998 JP 2000536855 PR 19-MAR-1998 IL 123758,01-SBP-1998 IL 126024 PI DAVID WALLACH,ANDREI KOVALENKO,MARSHALL S HORWITZ,YONGAN LI PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P29/00,A61P31/18, PC A61P35/00, PC C07K14/47,C07K16/18,C12N1/21,C12P21/02//C07K14/525,C07K14/715, PC C12N15/00, PC A61K37/02 CC Receptor function regulator for TNF/NGF receptor family and other proteins FH Key Location/Qualifiers FT source 1..2009 /organism='Homo sapiens (human)'. FT Location/Qualifiers 1..2009 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'					
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QY	131	CAGCCCTTCCCTGTGGATGAATAGGCACTCTCGAAGAGCCAACTGTGTGAGATGGTG	190	1211	GACATGAGGAAGCGGCTGTGAGGTCTCCAGGCCCCCTTGGCCCCCCTGCCTAC	1270
Db	136	CAGCCCTTCCCTGTGGATGAATAGGCACTCTCGAAGAGCCAACTGTGTGAGATGGTG	195	1216	GACATGAGGAAGCGGCTGTGAGGTCTCCAGGCCCCCTTGGCCCCCCTGCCTAC	1275
QY	191	CAGCCAGTGTGGCCCGCAGAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGG	250	1271	CTCTCTCTCCCTGGCCCTGCGCCAGCCAGAGAGGAGGCCCCCAGAGAGCCACTGAC	1330
Db	196	CAGCCAGTGTGGCCCGCAGAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGG	255	1276	CTCTCTCTCCCTGGCCCTGCGCCAGCCAGAGAGGAGGCCCCCAGAGAGCCACTGAC	1335
QY	251	AAGCCAGCCATCTGCACCTGCTTCAGAAACAGGGGCTCCTGAGACCCTCCAGCGCTGC	310	1331	TTCTGCTGTCCCAAGTGCAGTATCAGGCCCTCTGATATGGACACCTTCGAGATACATGTC	1390
Db	256	AAGCCAGCCATCTGCACCTGCTTCAGAAACAGGGGCTCCTGAGACCCTCCAGCGCTGC	315	1336	TTCTGCTGTCCCAAGTGCAGTATCAGGCCCTCTGATATGGACACCTTCGAGATACATGTC	1395
QY	311	CTGGAGGAGAAATCAAGAGTCCGAGATGCCATCCGGCAGAGCAACACAGATTCTGGGGAG	370	1391	ATGGAGTGCATTGAGTAGGGCCGGCCAGTGCAGGCCACTGCTG-CGAGGACGTGCC	1450
Db	316	CTGGAGGAGAAATCAAGAGTCCGAGATGCCATCCGGCAGAGCAACACAGATTCTGGGGAG	375	1396	ATGGAGTGCATTGAGTAGGGCCGGCCAGTGCAGGCCACTGCTG-CGAGGACGTGCC	1454
QY	371	CGCTGGAGAGTCTTCGATTTCAGCCAGCCAGAGGAGGAGAGAGTTCCTCATG	430	1451	GGGACCTGTGAGTCTGCGCTTCTCTCCGCTGCTAGCCAGAGTGAAGGGCTGGGT	1510
Db	376	CGCTGGAGAGTCTTCGATTTCAGCCAGCCAGAGGAGGAGAGAGTTCCTCATG	435	1455	GGGACCTGTGAGTCTGCGCTTCTCTCCGCTGCTAGCCAGAGTGAAGGGCTGGGT	1514
QY	431	TGCAAGTTCAGAGGCGCAGGAACTGGTGGAGAGACTCGGCTGGAGAGCTCCATCTG	490	1511	GGCCAACTGGGATGGCACTGGAGGCCCAACCCAGGAGCTGGCCCGGACCTTACGCT	1570
Db	436	TGCAAGTTCAGAGGCGCAGGAACTGGTGGAGAGACTCGGCTGGAGAGCTCCATCTG	495	1515	GGCCAACTGGGATGGCACTGGAGGCCCAACCCAGGAGCTGGCCCGGACCTTACGCT	1574
QY	491	AAGAGGCAAGAGGAGCAGGCTCTGGGGAGGTGGAGCACTCAAGAGATGCCAGAGCAG	550	1571	TCAGCTGTGTA-TCGCTGGTCCCTCTTTTGGGGTAGATGCGGCCCGGACCTCAGGCTGA	1629
Db	496	AAGAGGCAAGAGGAGCAGGCTCTGGGGAGGTGGAGCACTCAAGAGATGCCAGAGCAG	555	1575	TCAGCTGTGTA-TCGCTGGTCCCTCTTTTGGGGTAGATGCGGCCCGGACCTCAGGCTGA	1634
QY	551	ATGGCTGAGGACAAAGCCCTCTGTGAAAGCCAGGTGAGCTCTTGTCTGGGAGCTGAC	610	1630	CTCGTGTCTTTTGTTCCTTCTGTCTGTCTGCAACCACTTGGCTCGGGCTAATCCCTC	1689
Db	556	ATGGCTGAGGACAAAGCCCTCTGTGAAAGCCAGGTGAGCTCTTGTCTGGGAGCTGAC	615	1635	CTCGTGTCTTTTGTTCCTTCTGTCTGTCTGCAACCACTTGGCTCGGGCTAATCCCTC	1694

Qy	1690	CCTCTTCTCCACCGGCACTGGGGAAGTCAAGAAATGGGGCTCTGGGGCTCTCAGGGAGAA	1749	Db	496	AAGAGGAGAGAGGAGCAAGGCTCTCGGGAGGTGGAGCACTGAAAGAGATGCCAGCAGCAG	555
Db	1695	CCTCTTCTCCACCGGCACTGGGGAAGTCAAGAAATGGGGCTCTGGGGCTCTCAGGGAGAA	1754	Qy	551	ATGGCTGAGGACAAGGCTCTGTGAAAGCCAGGTGACGTCCTTGTGCTCGGGGAGCTGCAG	610
Qy	1750	CTGCTTCCCTCGCAGAGCTGGGTGGCAGCTTTCTCCACCGGACACCGACCGCCCGG	1809	Db	556	ATGGCTGAGGACAAGGCTCTGTGAAAGCCAGGTGACGTCCTTGTCTCGGGGAGCTGCAG	615
Db	1755	CTGCTTCCCTCGCAGAGCTGGGTGGCAGCTTTCTCCACCGGACACCGACCGCCCGG	1814	Qy	611	GAGAGCCAGAGTCTGCTTGGAGGCTGCCAATAAGGAATGCCAGGCTCTGAGGGGTCTGGGCC	670
Qy	1810	CCGCTGTGCCCTGGGAGTCTGCCCTCTTACCATGACACAGGCTGTCTCTCTTTGGGCT	1869	Db	616	GAGAGCCAGAGTCTGCTTGGAGGCTGCCAATAAGGAATGCCAGGCTCTGAGGGGTCTGGGCC	675
Db	1815	CTGCTGTGCCCTGGGAGTCTGCCCTCTTACCATGACACAGGCTGTCTCTCTTTGGGCT	1874	Qy	671	CGGCGGCGCAGCAGCAGCGCGGCGCAGCTGGAGAGTGGAGCGCGGCGCTGCAGCAGCAG	730
Qy	1870	GCATGCTATTCCATTTTGCAGCAGACCGATGTGATTAAACAGTCACTATTGATGGAC	1929	Db	676	CGGCGGCGCAGCAGCAGCGCGGCGCAGCTGGAGAGTGGAGCGCGGCGCTGCAGCAGCAG	735
Db	1875	GCATGCTATTCCATTTTGCAGCAGACCGATGTGATTAAACAGTCACTATTGATGGAC	1934	Qy	731	CACAGCGTGCAGGTGGACACAGCTGCGCATGCAGGGCCAGAGCGTGGAGGCGCGCTCCGC	790
Qy	1930	ATTTCGGTGTGTTCCCATCTTTTGTACCAATAAATGCGCATAGTAAAAA	1982	Db	736	CACAGCGTGCAGGTGGACACAGCTGCGCATGCAGGGCCAGAGCGTGGAGGCGCGCTCCGC	795
Db	1935	ATTTCGGTGTGTTCCCATCTTTTGTACCAATAAATGCGCATAGTAAAAA	1987	Qy	791	ATGGAGGCGCAGGCGCGCTCGAGGAGAAAGAGTGGCCCAAGTTGACGTTGACGTTGGGCTAT	850
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DEFINITION	Sequence 1 from Patent EP1454985.						
ACCESSION	Q0867779						
VERSION	Q0867779.1						
KEYWORDS	Homo sapiens (human)						
SOURCE	Homo sapiens						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1						
AUTHORS	Wallach,D. and Kovalenko,A.						
TITLE	Modulators of receptors of the tnfrngf receptor family						
JOURNAL	Patent: EP 1454985-A 1 08-SEP-2004;						
FEATURES	YEDA RESEARCH & DEVELOPMENT COMPANY, LTD. (IL)						
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	1..2009 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"						
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Query Match							
Best Local Similarity 99.6%; Score 1823; DB 6; Length 2009;							
Matches 1845; Conservative 3; Mismatches 3; Indels 2; Gaps 2;							
Qy	131	CAGCCCTTGGCCCTGTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGTG	190	Db	1211	GACATGAGGAAGCGGCATGTCCAGAGTCTCCAGGCCCCCTTGGCCCCCTTGGCTTAC	1270
Db	136	CAGCCCTTGGCCCTGTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGTG	195	Qy	1216	GACATGAGGAAGCGGCATGTCCAGAGTCTCCAGGCCCCCTTGGCCCCCTTGGCTTAC	1275
Qy	191	CAGCCAGTGTGGCCCGCAGCAGATCAGGACGTAATGCGGCGAGAGTCTCTCTGGGG	250	Db	1271	CT	1330
Db	196	CAGCCAGTGTGGCCCGCAGCAGATCAGGACGTAATGCGGCGAGAGTCTCTCTGGGG	255	Qy	1276	CT	1335
Qy	251	AAGCCAGCATGCTGTGCACTTCCAGAAACAGGGCGCTCTGAGACCTTCCAGAGCGTGC	310	Db	1331	TTCTGTCTGTCCAAAGTCCAGTATCAGGCCCCCTTGGCCCCCTTGGCTTAC	1390
Db	256	AAGCCAGCATGCTGTGCACTTCCAGAAACAGGGCGCTCTGAGACCTTCCAGAGCGTGC	315	Qy	1336	TTCTGTCTGTCCAAAGTCCAGTATCAGGCCCCCTTGGCCCCCTTGGCTTAC	1395
Qy	311	CTGGAGGAGATCAAGAGCTCCGAGTCCGATCCGCGAGAGCAACAGATTTCTGCGGAG	370	Db	1391	ATGGAGTGCATTGAGTGGGCGCGGCAGTGCAGAGCCACTTGCCTGCCCCAGGAGCGTCC	1450
Db	316	CTGGAGGAGATCAAGAGCTCCGAGTCCGATCCGCGAGAGCAACAGATTTCTGCGGAG	375	Qy	1451	GGGACCGTGCAGTCTGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1510
Qy	371	CGCTGCGAGGAGCTTCTGCACTTTCGAAGCCAGCCAGAGGAGGAGAGGATTTCTCATG	430	Db	1455	GGGACCGTGCAGTCTGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1514
Db	376	CGCTGCGAGAGCTTCTGCACTTTCGAAGCCAGCCAGAGGAGGAGAGGATTTCTCATG	435	Qy	1511	GGCCCAAACTGGGATGCCACCTGGAGCCCCACCCAGAGAGTGGCCCGGACCTTAGCT	1570
Qy	431	TGCAAGTTCCAGAGGCGAGGAACTCGTGGAGAGACTCGGCTGGAGAGCTCGATCTG	490	Db	1515	GGCCCAAACTGGGATGCCACCTGGAGCCCCACCCAGAGAGTGGCCCGGACCTTAGCT	1574
Db	436	TGCAAGTTCCAGAGGCGAGGAACTCGTGGAGAGACTCGGCTGGAGAGCTCGATCTG	495	Qy	1571	TCAGCTGTTGA-TCCGCTGGTCCCCTCTTTTGGGTFAGATGCGGCCCGCATCAGGCTGA	1629

Db 1575 TCAGCTGTTGAATTCCTGCTGCTCCCTCTCTTTTGGGGTAGATGCGGCCCGATCAGGCTGGA 1634
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Qy 1810 CCGCTGTCCTCGGAGTGTGCGCTCTTACCATGACACCGGTGCTCTCTTTTGGGCT 1869
Db 1815 CTGCTGTCCTCGGAGTGTGCGCTCTTACCATGACACCGGTGCTCTCTTTTGGGCT 1874
Qy 1870 GCATGCTATTCCATTTTGCAGCAGACCGATGTATTTAACCACTCACTATTGATGGAC 1929
Db 1875 GCATGCTATTCCATTTTGCAGCAGACCGATGTATTTAACCACTCACTATTGATGGAC 1934
Qy 1930 ATTTGGGTTGTTCCCATCTTTTGTATACCAATAAATAGGCATAGTAAAAA 1982
Db 1935 ATTTGGGTTGTTCCCATCTTTTGTATACCAATAAATAGGCATAGTAAAAA 1987

RESULT 11
AR534835
LOCUS AR534835 2009 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6734174.
ACCESSION AR534835
VERSION AR534835.1 GI:53925507
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2009)
AUTHORS Wallach,D., Kovalenko,A., Horwitz,M.S. and Li,Y.
TITLE Modulators of the function of receptors of the TNF/NGF receptor
JOURNAL Patent: US 6734174-A 11-MAY-2004;
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Location/Qualifiers
source 1..2009
/organism="unknown"
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ORIGIN
Query Match 91.4%; Score 1823; DB 6; Length 2009;
Best Local Similarity 99.6%; Pred. No. 1.2e-296;
Matches 1845; Conservative 3; Mismatches 3; Indels 2; Gaps 2;
Qy 131 CAGCCCTTGCCTGTTGGATGAATAGGCACCTCTGGAGAGCCAACTGTGTAGATGGTG 190
Db 136 CAGCCCTTGCCTGTTGGATGAATAGGCACCTCTGGAGAGCCAACTGTGTAGATGGTG 195
Qy 191 CAGCCAGTGTGGCCCGGACAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGG 250
Db 196 CAGCCAGTGTGGCCCGGACAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGG 255
Qy 251 AAGCCAGCATCTGCACCTGCTTTCAGAAACAGGGCGCTCTCAGACCCCTCCAGCGCTGC 310
Db 256 AAGCCAGCATCTGCACCTGCTTTCAGAAACAGGGCGCTCTCAGACCCCTCCAGCGCTGC 315
Qy 311 CTGGAGGAGAAATCAAGAGCTCCGATGCCATCCGCGAGAGCAACAGATTTCTGGGGAG 370
Db 316 CTGGAGGAGAAATCAAGAGCTCCGATGCCATCCGCGAGAGCAACAGATTTCTGGGGAG 375
Qy 371 CGCTGGAGAGCTTCTGCAATTTCAAGCCAGCAGAGGAGAGAGAGTTCCTCATG 430
Db 376 CGCTGGAGAGCTTCTGCAATTTCCAGCCAGCAGAGGAGAGAGAGTTCCTCATG 435
Qy 431 TCAGAGTTCAGAGGCGCCAGAAATCTGTTGGAGAGACTCGGCTTGGAGAGCTCGATCTG 490

Db 436 TGCAAGTTTCAGAGGCGCCAGGAAACTGTGTGGAGAGACTCGGCTTGGAGAAAGCTCGATCTG 495
Qy 491 AAGAGGCGAAGAGGAGCAGGCTCTCGGGGAGGTGGAGCACCTGAAGAGATGCGAGAGCAG 550
Db 496 AAGAGGCGAAGAGGAGCAGGCTCTCGGGGAGGTGGAGCACCTGAAGAGATGCGAGAGCAG 555
Qy 551 ATGGCTGAGGACAAGGCTCTGTGAAAGCCCAAGGTGACCTCTTGTCTGGGGAGCTGCGAG 610
Db 556 ATGGCTGAGGACAAGGCTCTGTGAAAGCCCAAGGTGACCTCTTGTCTGGGGAGCTGCGAG 615
Qy 611 GAGAGCAGAGTCTGCTTGGAGGCTGCCACTAAGGAATGCGAGGCTCTGAGAGGTTCGGGCC 670
Db 616 GAGAGCAGAGTCTGCTTGGAGGCTGCCACTAAGGAATGCGAGGCTCTGAGAGGTTCGGGCC 675
Qy 671 CGGGCGGCGAGCAGCGCGGAGCTGAGAGTGTAGCGGAGGCTGAGCGAGGCTGCGAGAGCAG 730
Db 676 CGGGCGGCGAGCAGCGCGGAGCTGAGAGTGTAGCGGAGGCTGAGCGAGGCTGCGAGAGCAG 735
Qy 731 CACAGCGTGCAGGTGGACCCAGCTGCGCATGCAAGGCGCAGAGCGTGGAGGCCGCTCCGC 790
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JOURNAL
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BD135432 2034 bp DNA linear PAT 18-SEP-2002
Receptor function regulator for TNF/NGF receptor family and other proteins.
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JP 2002506644-A/2.
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1 (bases 1 to 2034)
Wallach,D., Kovalenko,A., Horwitz,M.S. and Li,Y.
Receptor function regulator for TNF/NGF receptor family and other proteins
Patent: JP 2002506644-A 2 05-MAR-2002;
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LOCUS
DEFINITION Sequence 2 from patent US 6734174.

ACCESSION AR534836
VERSION AR534836.1 GI:53925508
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2034)
AUTHORS Wallach,D., Kovalenko,A., Horwitz,M.S. and Li,Y.
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QY 1692 TCTTCTCCACCCGCGACTGGGGAAGTCAAGAAATGGGGCTTGGGGCTCTCAGGGAGAACT 1751
Db 1728 TCTTCTCCACCCGCGACTGGGGAAGTCAAGAAATGGGGCTTGGGGCTCTCAGGGAGAACT 1787
QY 1752 GCTTCCCTCGCAGAGCTGGGTGGCAGCTTTCTCTCCACCGGACACCGACCCGCCCCGCC 1811
Db 1788 GCTTCCCTCGCAGAGCTGGGTGGCAGCTTTCTCTCCACCGGACACCGACCCGCCCCGCC 1847
QY 1812 GCTGTGCCCTGGGAGTGTGCCCTCTTACCATGACACAGGGTGTCTCTTTTGGGCTGC 1871
Db 1848 GCTGTGCCCTGGGAGTGTGCCCTCTTACCATGACACAGGGTGTCTCTTTTGGGCTGC 1907
QY 1872 ATGCTATTCATTTTGCAGCAGACCGATGTATTTAAACCACTTATTTAGTGGACAT 1931
Db 1908 ATGCTATTCATTTTGCAGCAGACCGATGTATTTAAACCACTTATTTAGTGGACAT 1967
QY 1932 TTGGGTGTTTCCATCTTTTGTACCAATAATAATGGCATGATAAAA 1981
Db 1968 TTGGGTGTTTCCATCTTTTGTACCAATAATAATGGCATGATAAAA 2017

RESULT 2

US-09-646-403-1
; Sequence 1, Application US/09646403
; Patent No. 6734174
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR F1
; FILE REFERENCE: WALLACH=27
; CURRENT APPLICATION NUMBER: US/09/646,403
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: IL 123758
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: PCT/IL99/00158
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: IL 126024
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2009
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-646-403-1

Query Match 91.4%; Score 1823; DB 4; Length 2009;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1845; Conservative 3; Mismatches 3; Indels 2; Gaps 2;
QY 131 CAGCCCTTCCCTGTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGT 190
Db 136 CAGCCCTTCCCTGTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGT 195
QY 191 CAGCCAGTGTGGTGGCCCGGAGCAGATCAGGAGCTA CTGGGCGGAAGAGTCTCTCTGGG 250

196 DB CAGCCAGTGGTGGCCCGGAGCAGATCAGGACGTACTGGGCAAGAGTCTCCTCTGGGG 255
251 QY AAGCCAGCCATGTGACCTGCTTTCAGAACAGGGCGCTCCTCAGACCCCTCAGCCCTGC 310
256 DB AAGCCAGCCATGTGACCTGCTTTCAGAACAGGGCGCTCCTCAGACCCCTCAGCCCTGC 315
311 QY CTGGAGGAGAAATCAGAGCTCCAGAGTCCATCCGGCAGAGCAACAGAGTTCTGCGGGAG 370
316 DB CTGGAGGAGAAATCAGAGCTCCAGAGTCCATCCGGCAGAGCAACAGAGTTCTGCGGGAG 375
371 QY CGCTGAGAGAGCTTCTGATTTCCAAAGCCAGCAGAGGAGAGAGTTCTTCATG 430
376 DB CGCTGAGAGAGCTTCTGATTTCCAAAGCCAGCAGAGGAGAGAGTTCTTCATG 435
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491 QY AAGAGCCAGAGGAGCAGGCTCTGCGGGAGGTGGAGCACTGAAGAGATGCCAGCAGCAG 550
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551 QY ATGGCTGAGAGCAAGGCTCTGTGAAGCCAGGTGACGTCTTGTCTCGGGAGAGTGCAG 610
556 DB ATGGCTGAGAGCAAGGCTCTGTGAAGCCAGGTGACGTCTTGTCTCGGGAGAGTGCAG 615
611 QY GAGAGCCAGAGTCTGAGGCTGCCACTNAGGAATGCCAGGCTCTGAGAGGTGGGGC 670
616 DB GAGAGCCAGAGTCTGAGGCTGCCACTNAGGAATGCCAGGCTCTGAGAGGTGGGGC 675
671 QY CGGGCGGCAGCAGCAGGCGCGGAGCTGGAGAGTGAGCGGAGCGCTGCAGCAGCAG 730
676 DB CGGGCGGCAGCAGCAGGCGCGGAGCTGGAGAGTGAGCGGAGCGCTGCAGCAGCAG 735
731 QY CACAGCGTGAGGTGAGCAGCTGCGCATGCGAGGCGCAGAGCGTGAGAGCCCGCTCCGC 790
736 DB CACAGCGTGAGGTGAGCAGCTGCGCATGCGAGGCGCAGAGCGTGAGAGCCCGCTCCGC 795
791 QY ATGGAGCGGCGGCGGCTCGGAGGAGAGAGGAGCTGCCAGTTGAGGTGGCCTAT 850
796 DB ATGGAGCGGCGGCGGCTCGGAGGAGAGAGGAGCTGCCAGTTGAGGTGGCCTAT 855
851 QY CACCACTCTTCAAGAAATACGACACACATCAAGAGCAGCGTGTGGGCGAGTGAGCGG 910
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911 QY AAGCGAGGAATGAGCTGGAAGATCTCAACAGCAGCTCCAGCAGGCCCGAGAGGCCCTG 970
916 DB AAGCGAGGAATGAGCTGGAAGATCTCAACAGCAGCTCCAGCAGGCCCGAGAGGCCCTG 975
971 QY GTGGCCAAACAGGAGTGTGATAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1030
976 DB GTGGCCAAACAGGAGTGTGATAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1035
1031 QY ATGGAGACCGCTTCGGGTGTGAAGGCCCGAGGCGGATATCTCAAGCGGAGCTTCAGGCT 1090
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1091 QY GAGAGCAGGCGCGGAGAGTGTGGCCGAGAGAGAGGAGCTCTCAGGAGCAGCTGGAG 1150
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1151 QY CAGCTGAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGGAGTCCGCCAGGATCGAG 1210
1156 DB CAGCTGAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGGAGTCCGCCAGGATCGAG 1215
1211 QY GACATGAGGAAGCGGATGTGAGGTCTCCAGGCGGCTTCCAGGCGGCTTCCAGGCGGCTTAC 1270
1216 DB GACATGAGGAAGCGGATGTGAGGTCTCCAGGCGGCTTCCAGGCGGCTTCCAGGCGGCTTAC 1275
1271 QY CTCTCTCTCTCCCTGGCCCTGCGCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1330

1276 DB CTCTCTCTCTCCCTGGCCCTGCGCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1335
1331 QY TTCTGCTGTCCCAAGTGCAGTATCAGGCCCCCTGATATGACACACCTTGACATACATGTC 1390
1336 DB TTCTGCTGTCCCAAGTGCAGTATCAGGCCCCCTGATATGACACACCTTGACATACATGTC 1395
1391 QY ATGGAGTGCATTGAGTAGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1450
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1451 QY GGGACCGTGCAGTGTGCTCTCCGCTGCTAGCCAGAGATGAAGGGCTGGGT 1510
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1511 QY GGGCAAACTGGGATGCGGAGCCCACTGGAGCCCACTGGAGAGCTGGCGCGGCACTTACGCT 1570
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1571 QY TCAGCTGTGGA-TCCGCTGGTCCCTCTTTTGGGGTAGATGCGGGCCCGATCAGGGCTGA 1629
1575 DB TCAGCTGTGGA-TCCGCTGGTCCCTCTTTTGGGGTAGATGCGGGCCCGATCAGGGCTGA 1634
1630 QY CTGCTGTCTTTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1689
1635 DB CTGCTGTCTTTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1694
1690 QY CCTCTTCTCCACCGGCACTGGGAGTCAAGATGGGGCTGGGGCTCTCAGGGAGAA 1749
1695 DB CCTCTTCTCCACCGGCACTGGGAGTCAAGATGGGGCTGGGGCTCTCAGGGAGAA 1754
1750 QY CTGCTTCCCTGGCAGAGCTGGGTGGCAGCTCTTCTCCACCGGACACCGACCCGCGG 1809
1755 DB CTGCTTCCCTGGCAGAGCTGGGTGGCAGCTCTTCTCCACCGGACACCGACCCGCGG 1814
1810 QY CCGTGTGCTTGGAGTGTGCTCTTACCATGACACCGGCTGCTCTCTTTTGGGCT 1869
1815 DB CTGCTGTGCTTGGAGTGTGCTCTTACCATGACACCGGCTGCTCTCTTTTGGGCT 1874
1870 QY GCATCTATTTCATTTTGGCAGCAGCAGATGTATTAACCACTCATATTGATGGAC 1929
1875 DB GCATCTATTTCATTTTGGCAGCAGCAGATGTATTAACCACTCATATTGATGGAC 1934
1930 QY ATTTGGGTGTTTCCCATCTTTTGTACCAATAATAGGCATAGTAAAAA 1982
1935 DB ATTTGGGTGTTTCCCATCTTTTGTACCAATAATAGGCATAGTAAAAA 1987

RESULT 3

US-09-646-403-2
; Sequence 2, Application US/09646403
; Patent No. 6734174
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR P7
; FILE REFERENCE: WALLACH-27
; CURRENT APPLICATION NUMBER: US/09/646,403
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: IL 123758
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: PCT/IL99/00158
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: IL 126024
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-646-403-2


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; TYPE: DNA
; ORGANISM: VEBNA
US-09-130-114-1

Query Match
Best Local Similarity 6.9%; Score 137; DB 2; Length 5452;
Matches 380; Conservative 0; Mismatches 405; Indels 0; Gaps 0;

QY 475 GGAGAAAGCTTCGATCTGAAGAGGCAGAAAGAGCAGAGCTCTCGGGAGGTGGAGCACCTGAA 534
Db 2145 GCAGGAGCGGAGGGGCAGAGCAGAGGCGAGGCGCAGGAGCAGGAGGCGGCGAGGAGCAGGA 2086

QY 535 GAGATGCCAGCAGCAGATCGCTGAGACAAGGCCTCTGTGAAAGCCCAAGTGTACCTCTT 594
Db 2085 CGAGGGCCAGGAGGGGCAGAGGGGCAGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCA 2026

QY 595 GCTCGGGAGCTGTCAGGAGCAGAGTGTGTTGAGGCTGCCACTAAGAAATGCCAGGC 654
Db 2025 CGAGGAGGGGCAGGAGGGGCAGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGCA 1966

QY 655 TCTGAGGGGTTCGGGCCCGGGCCGAGCAGAGCAGGCGCGCAGCTGGAGAGTGGAGCGCA 714
Db 1965 GGGGCAGAGGGGCAGGAGCAGAGAGGGGCAGAGGGGCAGGAGGGGCAGGAGCAGGAGCAGGA 1906

QY 715 GGCCTGTCAGCAGCAGCAGCAGCTGTCAGGTGGACCAAGCTGCGCATGCGAGGGCCAGAGCGT 774
Db 1905 CGAGGGCAGGAGCAGGAGGAGGGGCAGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGG 1846

QY 775 GGAGGCGCGCTCCGATGTGAGCGGCAGCGCGCTCGAGAGGAGAGAGAAAGTGGCCCA 834
Db 1845 GCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGG 1786

QY 835 GTTTCAGGTGGCTTATCAGCTCTTCCAGAAATACGACCAACCATCAAGAGCAGCGT 894
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QY 895 GGTGGGCACTGAGCGGAAGCAGGAATGTCAGCTTGAAGATCTCAACAGCAGCTCCAGCA 954
Db 1725 CGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGG 1666

QY 955 GGCAGGAGGCGCTTGGTGGCCCAACAGAGAGGTGATCGATAGCTGAGAGGAGGAGCCCA 1014
Db 1665 GCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGA 1606

QY 1015 GCAGCACAAAGATTGTGATGAGACCGTTCCGGTGTCTGAAGGCCCGAGGCGGATCTACAA 1074
Db 1605 GAGGGGCAGGAGGGGCAGGAGCAGAGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGGGGCA 1546

QY 1075 GGCAGACTTCCAGGCTGAGGAGCAGGCCCGGAGAGCTTGGCCGAGAAAGAGGAGCTCCT 1134
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QY 1135 GCAGGAGCAGCTGAGCAGCTGAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGACGA 1194
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QY 1195 GTCCGCCAGATTCAGGAGATCAGGAGAGCGGCACTGTCAGAGTCTCCAGGGCCCCCTTGC 1254
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QY 1255 CCCCC 1259
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RESULT 11
US-09-647-344A-14/c
; Sequence 14, Application US/09647344A
; Patent No. 6586180
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong

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; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.PCT US
; CURRENT APPLICATION NUMBER: US/09/647,344A
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 14
; LENGTH: 8705
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pShuttle
US-09-647-344A-14

Query Match
Best Local Similarity 6.9%; Score 137; DB 4; Length 8705;
Matches 380; Conservative 0; Mismatches 405; Indels 0; Gaps 0;

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QY 535 GAGATGCCAGCAGCAGATCGCTGAGACAAGGCCTCTGTGAAAGCCCAAGTGTACCTCTT 594
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QY 595 GCTCGGGAGCTGTCAGGAGCAGCAGTGTGTTGAGGCTGCCACTAAGAAATGCCAGGC 854
Db 7890 CGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGA 7831

QY 655 TCTGAGGGGTTCGGGCCCGGGCCGAGCAGAGCAGGCGCGCAGCTGGAGAGTGGAGCGCA 714
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QY 835 GTTTCAGGTGGCTTATCAGCTCTTCCAGAAATACGACCAACCATCAAGAGCAGCGT 894
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QY 1195 GTCCGCCAGATTCAGGAGATCAGGAGAGCGGCACTGTCAGAGTCTCCAGGGCCCCCTTGC 1254
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QY 1255 CCCCC 1259
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-620-925-1

Query Match 6.9%; Score 137; DB 3; Length 9600;
Best Local Similarity 48.4%; Pred. No. 4e-20;
Matches 380; Conservative 0; Mismatches 405; Indels 0; Gaps 0;

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QY 535 GAGATGCCAGCAGCAGATGCTGAGGAGCAAGGCTCTGTGAAGCCAGGTCGTCCTT 594
DB 766 GGAGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 825
QY 595 GCTCGGGGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 654
DB 826 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 885
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DB 946 GGAGGGCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1005
QY 775 GGAGGCGCGCTCCGATGAGGCGGCGAGGCGGCTCGAGGAGGAGGAGGAGGAGGAGGAG 834
DB 1006 GCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1065
QY 835 GTTGCAGGTGGCTATCACCAGCTCTTCCAGGATACGACACCATCAAGAGAGCCT 894
DB 1066 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1125
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QY 1015 GCAGCACAAGATTGATGAGAGCGCTTCCGCTGCTGAAGGCGGAGGAGGAGGAGGAG 1074
DB 1246 GAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1305
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DB 1306 GGAGGGCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1365
QY 1135 GCAGGAGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1194
DB 1366 GCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1425
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DB 1426 GGCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1485
QY 1255 CCGCG 1259
DB 1486 CCGCG 1490

RESULT 14
US-07-884-811-15
Sequence 15, Application US/07884811
Patent No. 5316921
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R.
TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/884,811
FILING DATE: 19920518
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 755.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-884-811-15

Query Match 6.9%; Score 137; DB 1; Length 10596;
Best Local Similarity 48.4%; Pred. No. 4.1e-20;
Matches 380; Conservative 0; Mismatches 405; Indels 0; Gaps 0;

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QY 835 GTTGCAGGTGGCTATCACCAGCTCTTCAAGAAATACGACCAACCATCATCAAGAGAGCCT 894
DB 2600 GCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2659
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DB 2660 GGAGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2719
QY 955 GGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1014

GenCore version 5.1.6
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Published Applications NA:*

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- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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SUMMARIES

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3	1994	100.0	1994	17	US-10-628-841-3
4	1836.4	92.1	2035	10	US-09-863-049A-3
5	1832.6	91.9	1975	10	US-09-972-607-10
6	1832.6	91.9	1975	17	US-10-628-841-10
7	1823	91.4	2009	18	US-10-761-370-1
8	1757.2	88.1	2034	18	US-10-761-370-2
9	941	47.2	1104	18	US-10-792-063-4
10	940.4	47.2	1874	14	US-10-189-388-2
11	940.4	47.2	1874	17	US-10-408-305-2
					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 10, Appli
					Sequence 1, Appli
					Sequence 2, Appli
					Sequence 2, Appli

12	705.8	35.4	23106	10	US-09-863-049A-1	Sequence 1, Appli
13	486	24.4	486	18	US-10-792-063-8	Sequence 8, Appli
14	402.6	20.2	483	18	US-10-792-063-6	Sequence 6, Appli
C 15	277.6	13.9	2803	9	US-09-925-298-84	Sequence 84, Appli
C 16	277.6	13.9	2803	14	US-10-102-806-84	Sequence 84, Appli
C 17	262	13.1	337	18	US-10-793-032-18	Sequence 18, Appli
18	216	10.8	597	16	US-10-029-386-12702	Sequence 12702, A
19	212	10.6	236	10	US-09-918-995-2339	Sequence 2339, Ap
20	207.4	10.4	526	16	US-10-029-386-9802	Sequence 9802, Ap
21	207	10.4	211	16	US-10-029-386-26402	Sequence 26402, A
22	195.4	9.8	197	16	US-10-029-386-23602	Sequence 10, Appli
23	187	9.4	264	18	US-10-792-063-10	Sequence 3, Appli
24	137	6.9	1926	15	US-10-294-804-3	Sequence 3, Appli
25	137	6.9	1926	18	US-10-194-046-3	Sequence 14, Appli
C 26	137	6.9	8705	15	US-10-291-230-14	Sequence 14, Appli
C 27	137	6.9	8705	15	US-10-291-249-14	Sequence 14, Appli
C 28	137	6.9	8705	17	US-10-273-678-16	Sequence 16, Appli
C 29	137	6.9	9600	16	US-10-278-751-1	Sequence 1, Appli
C 30	137	6.9	10233	16	US-10-050-898-283	Sequence 283, App
C 31	137	6.9	10285	16	US-10-050-902-283	Sequence 24, Appli
C 32	137	6.9	10330	18	US-10-656-269-24	Sequence 22, Appli
C 33	137	6.9	10330	18	US-10-656-269-20	Sequence 20, Appli
C 34	137	6.9	10516	18	US-10-656-269-18	Sequence 18, Appli
C 35	137	6.9	10561	18	US-10-656-269-18	Sequence 45, Appli
C 36	137	6.9	10615	18	US-10-656-269-23	Sequence 23, Appli
C 37	137	6.9	10774	18	US-10-656-269-21	Sequence 21, Appli
C 38	137	6.9	10921	18	US-10-656-269-19	Sequence 19, Appli
C 39	137	6.9	10961	18	US-10-656-269-17	Sequence 17, Appli
C 40	137	6.9	11006	18	US-10-656-269-17	Sequence 46, Appli
C 41	137	6.9	11059	18	US-10-656-269-17	Sequence 7, Appli
C 42	137	6.9	11924	18	US-10-678-816-7	Sequence 6, Appli
C 43	137	6.9	12242	18	US-10-678-816-6	Sequence 15, Appli
C 44	133	6.7	1787	18	US-10-609-133-15	Sequence 1, Appli
C 45	130.8	6.6	3489	11	US-09-894-273-1	

ALIGNMENTS

RESULT 1

US-09-972-607-3
; Sequence 3, Application US/09972607
; Publication No. US20030105037A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION
; FILE REFERENCE: RTS-0191
; CURRENT APPLICATION NUMBER: US/09/972,607
; CURRENT FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (149)...(1408)
US-09-972-607-3

Query Match	100.0%;	Score 1994;	DB 10;	Length 1994;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1994;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GGCAGAGATGCGCCCTTGTGATCCAGTGGGAACTAAGGCCAGAGAAAGTGAGGACC	60	
Db	1	GGCAGAGATGCGCCCTTGTGATCCAGTGGGAACTAAGGCCAGAGAAAGTGAGGACC	60	
QY	61	CGCAGACTATCAATCCAGTCTTCCCTCACTCCCTGTGAGCTCTCCAGCATCATC	120	
Db	61	CGCAGACTATCAATCCAGTCTTCCCTCACTCCCTGTGAGCTCTCCAGCATCATC	120	
QY	121	GAGTCCCATCAGCCCTTGCCTTGTGATGAATAGGCACCTCTGGAAGACCACTGTG	180	

Db 121 GAGTCCCATCAGCCCTTGCCCTGTTGGATGAAATAGGCACTCTGGAAGAGCAACTGTG 180
Qy 181 TGAGATGGTGACCCAGTCAGTGGTGGCCCGCAGCAGATCAGGACGTACTTGGGCGAAGAGTC 240
Db 181 TGAGATGGTGACCCAGTCAGTGGTGGCCCGCAGCAGATCAGGACGTACTTGGGCGAAGAGTC 240
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Db 241 TCCTCTGGGGAGCCAGCCATGCTGCACTGCTGCTTCAAGACAGGGCGCTCTCTGAGACCT 300
Qy 301 CCAGCGCTGCTCGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGCAGAGCAACCCAGAT 360
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Qy 361 TCTGCGGAGCGCTGCGAGGAGCTTCTGCAATTTCAAGCCAGCCAGAGGGAGGAGGA 420
Db 361 TCTGCGGAGCGCTGCGAGGAGCTTCTGCAATTTCAAGCCAGCCAGAGGGAGGAGGA 420
Qy 421 GTTCTCATGTGCAAGTTCAGAGGCGCCAGGAACTGGTGGAGACTCGGCGCTGGAGAA 480
Db 421 GTTCTCATGTGCAAGTTCAGAGGCGCCAGGAACTGGTGGAGACTCGGCGCTGGAGAA 480
Qy 481 GCTCGATCTGAAGAGGCGAGAGCAGGCTCTGCGGAGAGTGGAGCACTGAAGAGATG 540
Db 481 GCTCGATCTGAAGAGGCGAGAGCAGGCTCTGCGGAGAGTGGAGCACTGAAGAGATG 540
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Db 781 CGCGCTCCGCATGAGCGCGCAGCGCGCTCGAGGAGAGAGAGTGGCCCAAGTTGCA 840
Qy 841 GGTGGCCTATCAGCAGCTTCCAAAGATAGCAACCAATCAAGAGCAGCGTGGTGGG 900
Db 841 GGTGGCCTATCAGCAGCTTCCAAAGATAGCAACCAATCAAGAGCAGCGTGGTGGG 900
Qy 901 CAGTGAGCGGAAGCAGGAGTACAGCTGGAAGATCTCAAGAGAGTCCAGAGGCGCGA 960
Db 901 CAGTGAGCGGAAGCAGGAGTACAGCTGGAAGATCTCAAGAGAGTCCAGAGGCGCGA 960
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Qy 1021 CAAGATTGTGATGAGACCGTTCGGTCTGAGGCCCGAGCGGATATCTCAAGAGCGGA 1080
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Qy 1081 CTTCCAGGCTGAGAGCGCGGAGAGCTGGCCGAGAGAGAGGCTCCCTGCGAGGA 1140
Db 1081 CTTCCAGGCTGAGAGCGCGGAGAGCTGGCCGAGAGAGAGGCTCCCTGCGAGGA 1140
Qy 1141 GCAGTGGAGCAGCTGCGAGAGGAGTACAGCAAACTGAAGCCAGCTGTGAGGAGTGGC 1200
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Qy 1201 CAGGATCCAGGACATGAGGAGCGGATGTGAGGTCCTCCAGGCGCTTGGCCCCCGC 1260

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Db 1561 ACCTTACGCTTCAGCTGTTGATCCGCTGGTCCCTCTTTTGGGGTAGATGGCGCCCGAT 1620
Qy 1621 CAGGCTGACTGCTGCTCTTTTGGTTCCTCTGCTGCTCGAACCACTTGGCTCGGC 1680
Db 1621 CAGGCTGACTGCTGCTCTTTTGGTTCCTCTGCTGCTCGAACCACTTGGCTCGGC 1680
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Qy 1981 AAAAAAAAAAAAAA 1994
Db 1981 AAAAAAAAAAAAAA 1994

RESULT 2

US-09-851-673-1
; Sequence 1, Application US/09851673
; Publication No. US20030165985A1
; GENERAL INFORMATION:
; APPLICANT: Derry, Jonathan
; APPLICANT: Fauslow, William
; APPLICANT: Dougall, William
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
; FILE REFERENCE: 3198
; CURRENT APPLICATION NUMBER: US/09/851,673
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (149)...(1405)
US-09-851-673-1

Query Match 100.0%; Score 1994; DB 10; Length 1994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCAGAGCATGGCCCTTGTATCCAGGTGGGAAACTAAGGCCAGAGAGTGGACC 60
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QY 1 GGCACAGCATGGCCCTTGTATCCAGGTGGGAAACTAAGGCCAGAGAGTGGACC 60
Db |||||
QY 61 CGCAGACTATCAATCCAGTCTCTTCCCTCACTCCCTGTGAAGCTCTCCAGCATCATC 120
Db |||||
QY 61 CGCAGACTATCAATCCAGTCTCTTCCCTCACTCCCTGTGAAGCTCTCCAGCATCATC 120
Db |||||
QY 121 GAGTCCCATACGCCCTTCCCTGTGGATGAATAGGCACCTCTGGAAGAGCAACTGTG 180
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QY 121 GAGTCCCATACGCCCTTCCCTGTGGATGAATAGGCACCTCTGGAAGAGCAACTGTG 180
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QY 1801 ACCCGCCCGCTGTGGCTGGGAGTGGTGGCTTCTTACCATGACACAGGCTGCTCTCC 1860
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QY 1861 TTTTGGGCTGCATGCTATTTCATTTTGCAGCCAGACCGAGTGTATTTAAACAGTCACTA 1920
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QY 1861 TTTTGGGCTGCATGCTATTTCATTTTGCAGCCAGACCGAGTGTATTTAAACAGTCACTA 1920
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QY 1921 TTGATGGAATTTGGGTTGTTTCCCATCTTTTGTGTAATTAATAGGATAGTAAAA 1980
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QY 1921 TTGATGGAATTTGGGTTGTTTCCCATCTTTTGTGTAATTAATAGGATAGTAAAA 1980
Db |||||
QY 1981 AAAAAAAAAAAAAA 1994
Db |||||
QY 1981 AAAAAAAAAAAAAA 1994
Db |||||

RESULT 3
US-10-628-841-3
; Sequence 3, Application US/10628841
; Publication No. US20040023918A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION
; FILE REFERENCE: RTS-0191
; CURRENT APPLICATION NUMBER: US/10/628,841
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/972,607
; PRIOR FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (149)...(1408)
US-10-628-841-3

Query Match 100.0%; Score 1994; DB 17; Length 1994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGCAGCAGATGGCCCTTGTGATCCAGGTGGGAACTAAGGCCCCAGAGAGTGGAGCC	60
DB	1	GGCAGCAGATGGCCCTTGTGATCCAGGTGGGAACTAAGGCCCCAGAGAGTGGAGCC	60
QY	61	CGGACAGATCAATCCCAAGTCTCTTCCCTCACCTCCCTGTGAAGCTCTCCAGCATCATC	120
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DB	121	GAGGTCCCATAGCCCTTGGCCCTGTGTGATGAATAGGCACCTCTGGAAGCCCAACTGTG	180
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QY	241	TCTCTGGGAAAGCCAGCATCTGACCTGCTTTCAGAAAGAGGCGCTCTCTGAGACCT	300
DB	241	TCTCTGGGAAAGCCAGCATCTGACCTGCTTTCAGAAAGAGGCGCTCTCTGAGACCT	300
QY	301	CCAGCGCTCTGGAGGAGATCAAGAGCTCGAGATGCCATCCGGCAGAGCAACAGAT	360
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QY	361	TCTGGGGAGCGCTCGAGGAGCTTCTGCATTTCCAGAGCCAGCCAGAGGAGGAGGA	420
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DB	421	GTTCTCATGTGCAAGTTCCAGAGGCCAGGAACTGTGTGAGAGACTCGGCTGGAGAA	480
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DB	481	GCTCGATCTGAGAGGAGAGGAGGAGGCTCTCGGGAGGTGAGACCTGTAAGAGATG	540
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DB	601	GGAGTGCAGAGAGCCAGAGTCTGTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGA	660
QY	661	GGGTGGGCGCGGCGGACGAGGAGGCGGCGAGCTGGAGAGTGGCGGCGCT	720
DB			

Db	661	GGGTGGGCGCGGCGGACGAGAGGCGCGGAGCTGGAGAGTGGAGCGAGCGCGCT	720
QY	721	GCAGCAGCAGCAGCGTGCAGGTGGACCAAGCTCGCATGCGAGGCCAGAGCGTGGAGGC	780
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QY	781	CGGCTCCGATGGAGGCCAGCGCGCTCGGAGAGAGAGGAGCTGGCCAGCTTGA	840
Db	781	CGGCTCCGATGGAGGCCAGCGCGCTCGGAGAGAGAGGAGCTGGCCAGCTTGA	840
QY	841	GGTGGCCTATCACCAAGTATCCAAAGATACGACCAACACATCAAGAGCAGCTGGTGG	900
Db	841	GGTGGCCTATCACCAAGTATCCAAAGTATACGACCAACACATCAAGAGCAGCTGGTGG	900
QY	901	CAGTGAGCGAAAGCGAGGAATGCAAGTGTGAAGATCTCAACAGCAGCTCCAGAGCGCGA	960
Db	901	CAGTGAGCGAAAGCGAGGAATGCAAGTGTGAAGATCTCAACAGCAGCTCCAGAGCGCGA	960
QY	961	GGAGGCCCTGTGGCCAAACAGGAGGTGATCGATAAGCTGAGAGGAGGCGGAGCAGA	1020
Db	961	GGAGGCCCTGTGGCCAAACAGGAGGTGATCGATAAGCTGAGAGGAGGCGGAGCAGA	1020
QY	1021	CAAGATGTGATGAGAGACCTTCCGCTGTGAAGGCCAGCGGATATCTACAAGCGCGA	1080
Db	1021	CAAGATGTGATGAGAGACCTTCCGCTGTGAAGGCCAGCGGATATCTACAAGCGCGA	1080
QY	1081	CTTCCAGGCTGAGAGGAGCGCCCGGAGAGCTGGCCGAGAGAGAGCTCTCTGCAGGA	1140
Db	1081	CTTCCAGGCTGAGAGGAGCGCCCGGAGAGCTGGCCGAGAGAGAGCTCTCTGCAGGA	1140
QY	1141	GCAGCTGGAGCAGCTGCAGAGGAGGTACACAACTGAAGGCCAGCTGTCAAGAGTGGC	1200
Db	1141	GCAGCTGGAGCAGCTGCAGAGGAGGTACACAACTGAAGGCCAGCTGTCAAGAGTGGC	1200
QY	1201	CAGGATCGAGGACATGAGAGGAGCGGATGTCGAGGTCTCCAGGCCCTTGGCCCCCGC	1260
Db	1201	CAGGATCGAGGACATGAGAGGAGCGGATGTCGAGGTCTCCAGGCCCTTGGCCCCCGC	1260
QY	1261	CCCTGCTTACCTCTCTCTCCCTTGGCCCTGCGGATGTCGAGGTCTCCAGGCCCTTGG	1320
Db	1261	CCCTGCTTACCTCTCTCTCCCTTGGCCCTGCGGATGTCGAGGTCTCCAGGCCCTTGG	1320
QY	1321	GCACCTGACTTCTGTGTCCCAAGTGCAGATATCAGGCCCTGATATGACACCTGCA	1380
Db	1321	GCACCTGACTTCTGTGTCCCAAGTGCAGATATCAGGCCCTGATATGACACCTGCA	1380
QY	1381	GATACATGTATGAGGTGATGAGTGGCCCGGCGAGTCAAGGCCACTGTGCTGCGCGA	1440
Db	1381	GATACATGTATGAGGTGATGAGTGGCCCGGCGAGTCAAGGCCACTGTGCTGCGCGA	1440
QY	1441	GGAGCTGCCGGGACCGTGCAGTCTGCGCTTCTCTCCGCTGCTAGCCAGGATGA	1500
Db	1441	GGAGCTGCCGGGACCGTGCAGTCTGCGCTTCTCTCCGCTGCTAGCCAGGATGA	1500
QY	1501	AGGGCTGGGTGGCCCAACTGGGATGCCACTGGAGCCCAACAGAGAGCTGGCCGGGC	1560
Db	1501	AGGGCTGGGTGGCCCAACTGGGATGCCACTGGAGCCCAACAGAGAGCTGGCCGGGC	1560
QY	1561	ACCTTACGCTTACGCTGTGATCCGCTGTGCTTCTTTGGGGTATGCGGCCCGAT	1620
Db	1561	ACCTTACGCTTACGCTGTGATCCGCTGTGCTTCTTTGGGGTATGCGGCCCGAT	1620
QY	1621	CAGGCTGACTGCTGCTCTTTTGTCTCTCTCTCCGCTGCTAGCCAGGATGA	1680
Db	1621	CAGGCTGACTGCTGCTCTTTTGTCTCTCTCTCCGCTGCTAGCCAGGATGA	1680
QY	1681	TAATCCCTCTCTTCTCCACCGCAGTGGGAAAGTCAAGAAATGGGGCTCTGGGGCTCT	1740
Db	1681	TAATCCCTCTCTTCTCCACCGCAGTGGGAAAGTCAAGAAATGGGGCTCTGGGGCTCT	1740
QY	1741	CAGGAGAGACTGCTTCTCTTCTGCGAGCTGGGTGGGAGTCTTCTCTCCACCGGACCG	1800
Db	1741	CAGGAGAGACTGCTTCTCTCTTCTGCGAGCTGGGTGGGAGTCTTCTCTCCACCGGACCG	1800

QY 1801 ACCCGCCCGCGCTGTGCTGGAGTGTGCTGCTTACCATGACACAGGCTGCTCTCC 1860
DB 1801 ACCCGCCCGCGCTGTGCTGGAGTGTGCTGCTTACCATGACACAGGCTGCTCTCC 1860
QY 1861 TTTTGGGCTGCATGTATTCATTTTTCAGCCAGACCGATGTGTATTTAACAGTCACTA 1920
DB 1861 TTTTGGGCTGCATGTATTCATTTTTCAGCCAGACCGATGTGTATTTAACAGTCACTA 1920
QY 1921 TTGATGGACATTTGGGTTGTTTCCCATCTTTTGTACCATATAATGGCATAGTAAAA 1980
DB 1921 TTGATGGACATTTGGGTTGTTTCCCATCTTTTGTACCATATAATGGCATAGTAAAA 1980
QY 1981 AAAAAAAAAAAAAA 1994
DB 1981 AAAAAAAAAAAAAA 1994

RESULT 4
US-09-863-049A-3
; Sequence 3. Application US/09863049A
; Publication No. US2003002055A1
; GENERAL INFORMATION:
; APPLICANT: Kenrick, Sue J.
; APPLICANT: Nelson, David L.
; APPLICANT: Aradhya, Swaroop
; APPLICANT: D'Urso, Michele
; APPLICANT: Woffendin, Hayley
; APPLICANT: Munnich, Arnold
; APPLICANT: Smahi, Aamee
; APPLICANT: Israel, Alain
; APPLICANT: Poustka, Annemarie
; APPLICANT: Lewis, Richard A
; APPLICANT: Levy, Moise
; APPLICANT: Heiss, Nina
; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Def
; FILE OF INVENTION: NFKAPPA B (NF-kB) Activation
; FILE REFERENCE: HO-P01961US1
; CURRENT APPLICATION NUMBER: US/09/863, 049A
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/206,223
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2035
; TYPE: DNA
; ORGANISM: Human
US-09-863-049A-3

Query Match 92.1%; Score 1836.4; DB 10; Length 2035;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 132 AGCCCTTGCCCTGTTGGATGAATAGGACCTCTGGAAGACCAACTGTGTGAGATGGTGC 191
DB 169 AGCCCTTGCCCTGTTGGATGAATAGGACCTCTGGAAGACCAACTGTGTGAGATGGTGC 228
QY 192 AGCCAGTGTGTCGCGGAGAGATCAGGACGTACTGGGGGAGAGTCTCTCTGGGGA 251
DB 229 AGCCAGTGTGTCGCGGAGAGATCAGGACGTACTGGGGGAGAGTCTCTCTGGGGA 288
QY 252 AGCCAGCATGTGCACTGCTTACAGACAGGCGCTCTGAGACCTCCAGCGTGC 311
DB 289 AGCCAGCATGTGCACTGCTTACAGACAGGCGCTCTGAGACCTCCAGCGTGC 348
QY 312 TGGAGGAGATCAAGAGCTCCGAGATGCCATCCGGCAGACCAACAGATTTCTGCGGGAGC 371
DB 349 TGGAGGAGATCAAGAGCTCCGAGATGCCATCCGGCAGACCAACAGATTTCTGCGGGAGC 408
QY 372 GCTGCGAGAGCTTCTGCAATTTCCAGCCAGGAGGAGAGAGGAGTCTCTCATGT 431
DB 409 GCTGCGAGAGCTTCTGCAATTTCCAGCCAGGAGGAGGAGGAGTCTCTCATGT 468

QY 432 GCAAGTTCAGGAGGCCAGGAACTGTGTGAGAGACTCGGCCCTGGAGAGCTCGATCTGA 491
DB 469 GCAAGTTCAGGAGGCCAGGAACTGTGTGAGAGACTCGGCCCTGGAGAGCTCGATCTGA 528
QY 492 AGAGGCAGAAAGAGAGAGGCTCTGCGGGAGGTGGAGCACTGAAAGATGCCAGCAGCAGA 551
DB 529 AGAGGCAGAAAGAGAGAGGCTCTGCGGGAGGTGGAGCACTGAAAGATGCCAGCAGCAGA 588
QY 552 TGGCTGAGGACAAGGCTCTGTGAAAGCCAGGTGACGTCTTGTCTCGGGAGCTGACGG 611
DB 589 TGGCTGAGGACAAGGCTCTGTGAAAGCCAGGTGACGTCTTGTCTCGGGAGCTGACGG 648
QY 612 AGAGCCAGAGTCTGTTGGAGGCTGCCACTTAAGGAATGCCAGGCTCTGGAAGGCTCGGGCCC 671
DB 649 AGAGCCAGAGTCTGTTGGAGGCTGCCACTTAAGGAATGCCAGGCTCTGGAAGGCTCGGGCCC 708
QY 672 GGGCGCCAGCAGAGCAGCGCGCAGCTGGAGAGTGAGCGCGAGGCGCTGCGAGCAGCAGC 731
DB 709 GGGCGCCAGCAGAGCAGCGCGCAGCTGGAGAGTGAGCGCGAGGCGCTGCGAGCAGCAGC 768
QY 732 ACAGCGTGCAGGTGACACAGCTGCGGATGCGAGGCGCAGAGCGTGGAGGCGCGCTCCGCA 791
DB 769 ACAGCGTGCAGGTGACACAGCTGCGGATGCGAGGCGCAGAGCGTGGAGGCGCGCTCCGCA 828
QY 792 TGGAGCGCCAGCGCCCTCGGAGGAGAGAGAACTGGSCCAGTTGCAAGTGGCCCTATC 851
DB 829 TGGAGCGCCAGCGCCCTCGGAGGAGAGAGAACTGGSCCAGTTGCAAGTGGCCCTATC 888
QY 852 ACCAGCTCTTCCAGGAATACGACAAACCATCAAGAGCAGAGCGTGGTGGGAGCTGAGCGGA 911
DB 889 ACCAGCTCTTCCAGGAATACGACAAACCATCAAGAGCAGAGCGTGGTGGGAGCTGAGCGGA 948
QY 912 AGCGAGGATGAGCTGGAAGTCTCAAACAGCAGCTCCAGCAGGCGCGAGGAGGCCCTGG 971
DB 949 AGCGAGGATGAGCTGGAAGTCTCAAACAGCAGCTCCAGCAGGCGCGAGGAGGCCCTGG 1008
QY 972 TGGCCAAACAGGAGTGTGATAGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1031
DB 1009 TGGCCAAACAGGAGTGTGATAGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1068
QY 1032 TGGAGACCGTTCCGGTGTCTGAAGGCGCCAGGCGGATATCTTACAGGCGGACTTCCAGGCTG 1091
DB 1069 TGGAGACCGTTCCGGTGTCTGAAGGCGCCAGGCGGATATCTTACAGGCGGACTTCCAGGCTG 1128
QY 1092 AGAGGCAGGCGCCGAGAGCTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1151
DB 1129 AGAGGCAGGCGCCGAGAGAGCTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1188
QY 1152 AGCTGCAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTCCAGGAGTGGCGCAGGATCGAGG 1211
DB 1189 AGCTGCAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTCCAGGAGTGGCGCAGGATCGAGG 1248
QY 1212 ACATGAGGAAGCGGATGTGAGAGTCTCCAGGCGCCCTTTCGCCCGCCCTCCCTGCTTACC 1271
DB 1249 ACATGAGGAAGCGGATGTGAGAGTCTCCAGGCGCCCTTTCGCCCGCCCTCCCTGCTTACC 1308
QY 1272 TCT 1331
DB 1309 TCT 1368
QY 1332 TCT 1391
DB 1369 TCT 1428
QY 1392 TGGAGTGCATTTAGGTAGGCGCGCCAGTGCAGAGGCACTGCTTGGCCGAGGAGCGTGGCCG 1451
DB 1429 TGGAGTGCATTTAGGTAGGCGCGCCAGTGCAGAGGCACTGCTTGGCCGAGGAGCGTGGCCG 1487
QY 1452 GGAGCGTGCAGTCTGCGCTTCT 1511
DB 1488 GGAGCGTGCAGTCTGCGCTTCT 1547

QY 1512 GCCAACACTGGATGACCTGGAGCCCAACAGGAGTGGCGGCGACCTTACGCTT 1571
 DB 1548 GCCAACACTGGATGACCTGGAGCCCAACAGGAGTGGCGGCGACCTTACGCTT 1607
 QY 1572 CAGCTGTGTATCGCTGGTCCCTCTTTTGGGTAGATGCGGCCCGCATCAGGCGCTGACT 1631
 DB 1608 CAGCTGTGTATCGCTGGTCCCTCTTTTGGGTAGATGCGGCCCGCATCAGGCGCTGACT 1667
 QY 1632 CGCTGCTCTTTTGTTCCTCTCTGCTGCTCGAACAATTGCTCGGGCTAATCCCTCCC 1691
 DB 1668 CGCTGCTCTTTTGTTCCTCTCTGCTGCTCGAACAATTGCTCGGGCTAATCCCTCCC 1727
 QY 1692 TCTTCTCCACCCCGCACTGGGCACTCAAGAAATGGGCTGGGCTCTCAGGGAGACT 1751
 DB 1728 TCTTCTCCACCCCGCACTGGGCACTCAAGAAATGGGCTGGGCTCTCAGGGAGAACT 1787
 QY 1752 GCTTCCCTGGCAGAGCTGGGTGGCAGCTCTTCTCCACCGGACAACCGGCCCGCCGCC 1811
 DB 1788 GCTTCCCTGGCAGAGCTGGGTGGCAGCTCTTCTCCACCGGACAACCGGCCCGCCGCC 1847
 QY 1812 GCTGTGCCCTGGAGTGGTCCCTCTTACCATGACACGGGTGCTCTCTTTTGGGCTGC 1871
 DB 1848 GCTGTGCCCTGGAGTGGTCCCTCTTACCATGACACGGGTGCTCTCTTTTGGGCTGC 1907
 QY 1872 ATGCTATTCCATTTTGCAGCAGACCGATGTGTATTAAACAGTCACTATTGATGGACAT 1931
 DB 1908 ATGCTATTCCATTTTGCAGCAGACCGATGTGTATTAAACAGTCACTATTGATGGACAT 1967
 QY 1932 TTGGGTGTTCCTATCTTTTGTACCAATAAATATGGCATAGPAAAAA 1981
 DB 1968 TTGGGTGTTCCTATCTTTTGTACCAATAAATATGGCATAGTAAAAA 2017

RESULT 5
 US-09-972-607-10
 ; Sequence 10, Application US/09972607
 ; Publication No. US20030105037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION
 ; FILE REFERENCE: R15-0191
 ; CURRENT APPLICATION NUMBER: US/09/972,607
 ; CURRENT FILING DATE: 2001-10-06
 ; NUMBER OF SEQ ID NOS: 88
 ; SEQ ID NO 10
 ; LENGTH: 1975
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (111)...(1370)
 US-09-972-607-10

Query Match 91.9%; Score 1832.6; DB 10; Length 1975;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1846; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 131 CAGCCCTTGCCTGTGGTGAATAGGACACCTCTGGAAGCCCACTGTGTGAGATGGT 190
 DB 93 CAGCCCTTGCCTGTGGTGAATAGGACACCTCTGGAAGCCCACTGTGTGAGATGGT 152
 QY 191 CAGCCAGTGTGGTGGCCGCGCAGCAGATCAGGACGTAATCTGGGCGAAGAGTCTCTCTGGGG 250
 DB 153 CAGCCAGTGTGGTGGCCGCGCAGCAGATCAGGACGTAATCTGGGCGAAGAGTCTCTCTGGGG 212
 QY 251 AAGCCAGCATGCTGCACCTTTCAGAAAGGCGCTCTGTGACACCTCCAGCGCTGC 310
 DB 213 AAGCCAGCATGCTGCACCTTTCAGAAAGGCGCTCTGTGACACCTCCAGCGCTGC 272
 QY 311 CTGGAGGAGATCAAGAGCTCCGAGATGCCATCCGGCAGACCAACAGATTTCTCGGGAG 370
 DB 273 CTGGAGGAGATCAAGAGCTCCGAGATGCCATCCGGCAGACCAACAGATTTCTCGGGAG 332

QY 371 CGCTGCGAGGAGCTTCTGCAATTTCAAAGCCAGCAGAGGAGGAGAGTTCCTCATG 430
 DB 333 CGCTGCGAGGAGCTTCTGCAATTTCAAAGCCAGCAGAGGAGGAGAGTTCCTCATG 392
 QY 431 TGCAGTTTCCAGGAGGACGAAACTGGTGGAGAGACTCGGCTTGGAGAGCTCATCTG 490
 DB 393 TGCAGTTTCCAGGAGGACGAAACTGGTGGAGAGACTCGGCTTGGAGAGCTCATCTG 452
 QY 491 AAGAGGCGAGAGGAGCAGAGGCTCTCGGAGAGTGGAGCACTTGAAGAGATGCCAGCAGCAG 550
 DB 453 AAGAGGCGAGAGGAGCAGAGGCTCTCGGAGAGTGGAGCACTTGAAGAGATGCCAGCAGCAG 512
 QY 551 ATGCTGAGGACAAAGGCTCTGTGAAAGCCAGAGTGGAGTCTTGTCTCGGAGAGCTGAG 610
 DB 513 ATGCTGAGGACAAAGGCTCTGTGAAAGCCAGAGTGGAGTCTTGTCTCGGAGAGCTGAG 572
 QY 611 GAGAGCCAGAGTCCGTTGGAGGCTGCCAATAAGCAATGCCAGGCTCTGAGAGGTCGGGCC 670
 DB 573 GAGAGCCAGAGTCCGTTGGAGGCTGCCAATAAGCAATGCCAGGCTCTGAGAGGTCGGGCC 632
 QY 671 CGGCGCCCAAGCAGAGCGCGCAGCTGGAGAGTGGAGCGCAGGCGCTGCGAGCAGCAG 730
 DB 633 CGGCGCCCAAGCAGAGCGCGCAGCTGGAGAGTGGAGCGCAGGCGCTGCGAGCAGCAG 692
 QY 731 CACAGCGTCAGAGTGGACCAAGCTCGCATGCGAGGCGCAGAGCGTGGAGCGCGCTCGCG 790
 DB 693 CACAGCGTCAGAGTGGACCAAGCTCGCATGCGAGGCGCAGAGCGTGGAGCGCGCTCGCG 752
 QY 791 ATGAGCGCCAGCGCGCTCGAGGAGAGAGGAACTGGCCCACTGAGTTCAGGTGCGCTAT 850
 DB 753 ATGAGCGCCAGCGCGCTCGAGGAGAGAGGAACTGGCCCACTGAGTTCAGGTGCGCTAT 812
 QY 851 CACAGCTCTTCCAAGAAATACGACAACCATCAAGAGCAGCGTGGTGGCAGTAGCGG 910
 DB 813 CACAGCTCTTCCAAGAAATACGACAACCATCAAGAGCAGCGTGGTGGCAGTAGCGG 872
 QY 911 AAGCGGAATGCACTGGAGTCTTCAACAGCAGCTCCAGCAGGCGCGGAGGCGCTG 970
 DB 873 AAGCGGAATGCACTGGAGTCTTCAACAGCAGCTCCAGCAGGCGCGGAGGCGCTG 932
 QY 971 GTGCCCAAAACAGGAGTGTATGATGCTGAAGGAGGAGGCGGAGCAGCAGCAAGATTGTG 1030
 DB 933 GTGCCCAAAACAGGAGTGTATGATGCTGAAGGAGGAGGCGGAGCAGCAGCAAGATTGTG 992
 QY 1031 ATGAGACCGTTCCGCTGTGAAGGCGCAGCGGATATCTTACAAGGCGGACTTCCAGGCT 1090
 DB 993 ATGAGACCGTTCCGCTGTGAAGGCGCAGCGGATATCTTACAAGGCGGACTTCCAGGCT 1052
 QY 1091 GAGAGCGAGCGCGGAGAGCTGGCGGAGAGAGGAGCTCTGCGAGGAGCAGCTGAG 1150
 DB 1053 GAGAGCGAGCGCGGAGAGCTGGCGGAGAGAGGAGCTCTGCGAGGAGCAGCTGAG 1112
 QY 1151 CAGCTCAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTGAGGAGTGGCGCAGGATCGAG 1210
 DB 1113 CAGCTCAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTGAGGAGTGGCGCAGGATCGAG 1172
 QY 1211 GACATGAGGAGCGGCTATGCGAGTCTCCAGGCGCGCTTGGCGCGCGCTGCGCTAC 1270
 DB 1173 GACATGAGGAGCGGCTATGCGAGTCTCCAGGCGCGCTTGGCGCGCGCTGCGCTAC 1232
 QY 1271 CT 1330
 DB 1233 CT 1292
 QY 1331 TTCTGTCT 1390
 DB 1293 TTCTGTCT 1352
 QY 1391 ATGAGTGTGATTGAGTGGCGCGGCTGAGGCGCAGTGCAGAGGCGCTGCGCGGAGGCTGCC 1450
 DB 1353 ATGAGTGTGATTGAGTGGCGCGGCTGAGTGCAGAGGCGCTGCGCGGAGGCTGCC 1411

QY 1451 GGACCGTGCAGTCTGGCTTTCTCTCCCGCTGCTAGCCAGGATGAAGGCTGGGT 1510
DB 1412 GGACCGTGCAGTCTGGCTTTCTCTCCCGCTGCTAGCCAGGATGAAGGCTGGGT 1471
QY 1511 GGCCAACTGGGATGCCACTGGAGCCCAACCCAGAGAGTGGCCGGGACCTTAGCCT 1570
DB 1472 GGCCAACTGGGATGCCACTGGAGCCCAACCCAGAGAGTGGCCGGGACCTTAGCCT 1531
QY 1571 TCAGCTGTGTGATCGCTGGTCCCTCTTTTGGGTAGATCGGCCCGGATCAGGCTGAC 1630
DB 1532 TCAGCTGTGTGATCGCTGGTCCCTCTTTTGGGTAGATCGGCCCGGATCAGGCTGAC 1591
QY 1631 TCCTGTCTTTTGTTCCTCTCTGTCTGCTCGAACCACTTGCTCGGGCTAATCCCTCC 1690
DB 1592 TCCTGTCTTTTGTTCCTCTCTGTCTGCTCGAACCACTTGCTCGGGCTAATCCCTCC 1651
QY 1691 CTCTTCTCCACCGGCACTGGGGAGTCAAGAAATGGGGCTGGGCTCTCAGGGAGAAC 1750
DB 1652 CTCTTCTCCACCGGCACTGGGGAGTCAAGAAATGGGGCTGGGCTCTCAGGGAGAAC 1711
QY 1751 TGCTTCCCTTGGCAGAGTGGGTGGCAGCTCTTCTCCACCGGACACCGGCCCGCC 1810
DB 1712 TGCTTCCCTTGGCAGAGTGGGTGGCAGCTCTTCTCCACCGGACACCGGCCCGCC 1771
QY 1811 CGCTGTCCCTTGGGAGTGTGCTCTTACCATGACACGGGTGCTCTCTTTTGGGCTG 1870
DB 1772 CGCTGTCCCTTGGGAGTGTGCTCTTACCATGACACGGGTGCTCTCTTTTGGGCTG 1831
QY 1871 CATGCTATTCCATTTTGCAGCCAGACCGATGTATTTAACAGTCACTATTGATGGACA 1930
DB 1832 CATGCTATTCCATTTTGCAGCCAGACCGATGTATTTAACAGTCACTATTGATGGACA 1891
QY 1931 TTTGGGTGTGTTCCCATCTTTTGTGTACCATAAATATGSCATAGTAAAAA 1981
DB 1892 TTTGGGTGTGTTCCCATCTTTTGTGTACCATAAATATGSCATAGTAAAAA 1942

RESULT 6

US-10-628-841-10
; Sequence 10, Application US/10628841
; Publication No. US20040023918A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION
; FILE REFERENCE: RTS-0191
; CURRENT APPLICATION NUMBER: US/10/628,841
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/972,607
; PRIOR FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 1975
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (111)...(1370)
US-10-628-841-10

Query Match 91.9%; Score 1832.6; DB 17; Length 1975;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1846; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 131 CAGCCCTTGCCTTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGTG 190
DB 93 CAGCCCTTGCCTTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGTG 152
QY 191 CAGCCAGTGTGGCCCGCAGCAGATCAGGACGTCTGGCGGAGAGTCTCTCTTGGGG 250
DB 153 CAGCCAGTGTGGCCCGCAGCAGATCAGGACGTCTGGCGGAGAGTCTCTCTTGGGG 212
QY 251 AAGCCAGCCATGTGCACCTTGCTTTCAGAAACAGGGCGCTCCTGAGACCCTCCAGCGCTGC 310

DB 213 AAGCCAGCCATGTGCACCTTGCTTTCAGAAACAGGGCGCTCCTGAGACCCTCCAGCGCTGC 272
QY 311 CTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACAGATTTCTGGGGAG 370
DB 273 CTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACAGATTTCTGGGGAG 332
QY 371 CGCTGCGAGGAGCTTCTGCAATTTCCAAAGCCAGCCAGAGGAGGAGAGGATTCCTCATG 430
DB 333 CGCTGCGAGGAGCTTCTGCAATTTCCAAAGCCAGCCAGAGGAGGAGAGGATTCCTCATG 392
QY 431 TGCAGGTTCCAGGAGGCCAGGAACTGTGTGGAGAGACTCGGCCCTGGAGAACTCGATCTG 490
DB 393 TGCAGGTTCCAGGAGGCCAGGAACTGTGTGGAGAGACTCGGCCCTGGAGAACTCGATCTG 452
QY 491 AAGAGCCAGAGGAGCAGGAGCTCTGCGGAGGTGGAGACACTGGAAGATGTCAGAGCAG 550
DB 453 AAGAGCCAGAGGAGCAGGAGCTCTGCGGAGGTGGAGACACTGGAAGATGTCAGAGCAG 512
QY 551 ATGGCTGAGGACAAAGGCTCTGTGAAGCCAGGTGACGTCTTGTCTCGGGAGCTGCAG 610
DB 513 ATGGCTGAGGACAAAGGCTCTGTGAAGCCAGGTGACGTCTTGTCTCGGGAGCTGCAG 572
QY 611 GAGAGCCAGAGTCTGAGGCTGCTCACTAAGGAATGCGAGGCTCTGAGAGGTCCGGGCC 670
DB 573 GAGAGCCAGAGTCTGAGGCTGCTCACTAAGGAATGCGAGGCTCTGAGAGGTCCGGGCC 632
QY 671 CCGGGCCAGCAGCAGCAGCGCGGAGTGTGAGAGTGTGAGCGGAGCGCTGTGAGCAGCAG 730
DB 633 CCGGGCCAGCAGCAGCAGCGCGGAGTGTGAGAGTGTGAGCGGAGCGCTGTGAGCAGCAG 692
QY 731 CACAGGTGACGTGTGAGCAGCTGCGCATGCAAGGCCAGAGCGTGTGAGCGCCGCTCCGC 790
DB 693 CACAGGTGACGTGTGAGCAGCTGCGCATGCAAGGCCAGAGCGTGTGAGCGCCGCTCCGC 752
QY 791 ATGGAGCGCCAGCGCCCTCGGAGGAGAAAGAGAACTGCGCCAGTTGAGAGTGGCTAT 850
DB 753 ATGGAGCGCCAGCGCCCTCGGAGGAGAAAGAGAACTGCGCCAGTTGAGAGTGGCTAT 812
QY 851 CACAGCTCTTCAAGATATCAACAAACACATCAAGAGCAGCGTGTGTGGCAGTGAAGCGG 910
DB 813 CACAGCTCTTCAAGATATCAACAAACACATCAAGAGCAGCGTGTGTGGCAGTGAAGCGG 872
QY 911 AAGCCAGGAATCAGCTGGAAGATCTCAAAACAGCAGCTTCAAGCAGCCCGAGAGGCCCTG 970
DB 873 AAGCCAGGAATCAGCTGGAAGATCTCAAAACAGCAGCTTCAAGCAGCCCGAGAGGCCCTG 932
QY 971 GTGGCCAAACAGGAGGTGATTCGATTAAGCTGAAGGAGGAGCGGAGCAGCAAGATTTGTG 1030
DB 933 GTGGCCAAACAGGAGGTGATTCGATTAAGCTGAAGGAGGAGCGGAGCAGCAAGATTTGTG 992
QY 1031 ATGGAGACCGTTCCGGTGTGAAGCCCAAGGCGGATATCTCAAGCGCACTTCCAGGCT 1090
DB 993 ATGGAGACCGTTCCGGTGTGAAGCCCAAGGCGGATATCTCAAGCGCACTTCCAGGCT 1052
QY 1091 GAGAGCGAGCCCGGAGAGCTGCGCCGAGAGAGGAGCTCTTGCAGAGCAGCTGGAG 1150
DB 1053 GAGAGCGAGCCCGGAGAGCTGCGCCGAGAGAGGAGCTCTTGCAGAGCAGCTGGAG 1112
QY 1151 CAGCTGTGAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGAGTTCGGCCAGGATTCGAG 1210
DB 1113 CAGCTGTGAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGAGTTCGGCCAGGATTCGAG 1172
QY 1211 GACATGAGAGCGGATGTTCAGGTCTCCAGGCCCTTCCGCCCTCCGCCCTTGCCTAC 1270
DB 1173 GACATGAGAGCGGATGTTCAGGTCTCCAGGCCCTTCCGCCCTCCGCCCTTGCCTAC 1232
QY 1271 CTCTCTCTCCCTCGCCCTGCCAGCAGAGGAGGAGCCCGCCCGAGAGGAGCCACTGAC 1330
DB 1233 CTCTCTCTCTCCCTCGCCCTGCCAGTCAAGAGGAGGAGCCCGCCCGAGAGGAGCCACTGAC 1292
QY 1331 TTCTCTCTGTCCCAAGTGCAGGTATCAGGCCCTGTATGGAACACCTCTGAGATATACATGTC 1390

Db 1293 TTCTGCTGCCAAGTCCAGTATCAGGCCCTGATATGACACCCCTGCAGATACATGTC 1352
 Qy 1391 ATGAGTGCATAGTAGGCGCGCAGTGCAGGCCACTGCTGCGCCGAGGACGTGCC 1450
 Db 1353 ATGAGTGCATAGTAGGCGCGCAGTGCAGGCCACTGCTG-CGAGGACGTGCC 1411
 Qy 1451 GGGACCGTGCAGTCCGCTTCTCCGCGCTGCTAGGCCAGGATGAGGGCTGGT 1510
 Db 1412 GGGACCGTGCAGTCCGCTTCTCCGCGCTGCTAGGCCAGGATGAGGGCTGGT 1471
 Qy 1511 GGGACCAACTGGATGCCACTGGAGCCCAACCCAGGAGCTGGCGCGGCACTTACGCT 1570
 Db 1472 GGGACCAACTGGATGCCACTGGAGCCCAACCCAGGAGCTGGCGCGGCACTTACGCT 1531
 Qy 1571 TCAGCTGTTGATCCGCTGGTCCCTCTTTGGGGTAGATGCGGCCCGGATCAGGCTGAC 1630
 Db 1532 TCAGCTGTTGATCCGCTGGTCCCTCTTTGGGGTAGATGCGGCCCGGATCAGGCTGAC 1591
 Qy 1631 TCAGCTGCTCTTTTGTTCCTCTGCTGCTCGAACCACTTGCCTCGGCGCTAATCCCTCC 1690
 Db 1592 TCAGCTGCTCTTTTGTTCCTCTGCTGCTCGAACCACTTGCCTCGGCGCTAATCCCTCC 1651
 Qy 1691 CTCTTCTCCACCCGCACTGGGGAGTCAAGAAATGGGGCTTCCAGGAGAAC 1750
 Db 1652 CTCTTCTCCACCCGCACTGGGGAGTCAAGAAATGGGGCTTCCAGGAGAAC 1711
 Qy 1751 TGCTTCCCTGGCAGAGCTGGTGGAGCTCTTCTCCAGCCACTTGCCTCGGCGCTAATCCCTCC 1810
 Db 1712 TGCTTCCCTGGCAGAGCTGGTGGAGCTCTTCTCCAGCCACTTGCCTCGGCGCTAATCCCTCC 1771
 Qy 1811 CGCTGTCCTGGAGTGTGCTCTTACCATGCACACGGGTGCTCTCTTTGGGGCTG 1870
 Db 1772 CGCTGTCCTGGAGTGTGCTCTTACCATGCACACGGGTGCTCTCTTTGGGGCTG 1831
 Qy 1871 CATGCTATTCATTTTGACGACGACCGATGATTAATTAACAGTCACTATTGATGACA 1930
 Db 1832 CATGCTATTCATTTTGACGACGACCGATGATTAATTAACAGTCACTATTGATGACA 1891
 Qy 1931 TTTGGGTGTTTCCCATCTTTTGTACCATAAATAGGCATAGTAAAA 1981
 Db 1892 TTTGGGTGTTTCCCATCTTTTGTACCATAAATAGGCATAGTAAAA 1942

RESULT 7

US-10-761-370-1
 ; Sequence 1, Application US/10761370
 ; Publication No. US20040219615A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WALLACH, David
 ; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR F
 ; TITLE OF INVENTION: AND OTHER PROTEINS
 ; FILE REFERENCE: WALLACH-27
 ; CURRENT APPLICATION NUMBER: US/10/761,370
 ; CURRENT FILING DATE: 2004-01-22
 ; PRIOR APPLICATION NUMBER: US/09/646,403
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: IL 123758
 ; PRIOR FILING DATE: 1998-03-19
 ; PRIOR APPLICATION NUMBER: PCT/IL99/00158
 ; PRIOR FILING DATE: 1999-03-18
 ; PRIOR APPLICATION NUMBER: IL 126024
 ; PRIOR FILING DATE: 1998-09-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 2009
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-761-370-1

Query Match 91.4%; Score 1823; DB 18; Length 2009;
 Best Local Similarity 99.6%; Pred. No. 0;

Matches 1845; Conservative 3; Mismatches 3; Indels 2; Gaps 2;
 Qy 131 CAGCCCTTGCCTCTTGGATGAATAGGCACCTCTTGAAGAGCACTGTGTGATGATGTTG 190
 Db 136 CAGCCCTTGCCTCTTGGATGAATAGGCACCTCTTGAAGAGCACTGTGTGATGATGTTG 195
 Qy 191 CAGCCCAAGTGTGTCGCGCGAGCAGATCAGACGCTACTTGGGCGAAGAGTCTCTCTGGGG 250
 Db 196 CAGCCCAAGTGTGTCGCGCGAGCAGATCAGACGCTACTTGGGCGAAGAGTCTCTCTGGGG 255
 Qy 251 AAGCCAGCCTAGTGCACCTTCCAGAACAGGCGCTCTGAGACCTCCAGCGCTGC 310
 Db 256 AAGCCAGCCTAGTGCACCTTCCAGAACAGGCGCTCTGAGACCTCCAGCGCTGC 315
 Qy 311 CTGAGGAGGAATCAAGAGCTCCGAGATGCTCCGCGAGCAACACAGATTCTCGGGAG 370
 Db 316 CTGAGGAGGAATCAAGAGCTCCGAGATGCTCCGCGAGCAACACAGATTCTCGGGAG 375
 Qy 371 CGCTGCGAGGAGCTTCTGCATTTCCAAAGCAGCAGAGGAGGAGAGGATTCCTCATG 430
 Db 376 CGCTGCGAGGAGCTTCTGCATTTCCAAAGCAGCAGAGGAGGAGAGGATTCCTCATG 435
 Qy 431 TGCAAGTTCCAGGAGGCGCAGGAACTCGTGGAGAGACTCGGCCTGGAGAGCTCGATCTG 490
 Db 436 TGCAAGTTCCAGGAGGCGCAGGAACTCGTGGAGAGACTCGGCCTGGAGAGCTCGATCTG 495
 Qy 491 AAGAGCAGAAAGAGAGGCTCTGCGGAGGTGGAGCACTTGAAGAGATGCCAGCAGCAG 550
 Db 496 AAGAGCAGAAAGAGAGGCTCTGCGGAGGTGGAGCACTTGAAGAGATGCCAGCAGCAG 555
 Qy 551 ATGCTCAGACGACAGGCTCTGTGAAGCCAGCTGAGCTCTTCTCGGGAGGAGTGCAG 610
 Db 556 ATGCTCAGACGACAGGCTCTGTGAAGCCAGCTGAGCTCTTCTCGGGAGGAGTGCAG 615
 Qy 611 GAGAGCCAGAGTCTGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGAGGGTCCGGCC 670
 Db 616 GAGAGCCAGAGTCTGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGAGGGTCCGGCC 675
 Qy 671 CGGGCGCCAGCAGCAGGCGCGGCACTGGAGAGTGAAGGAGGCGCTCGAGCAGCAG 730
 Db 676 CGGGCGCCAGCAGCAGGCGCGGCACTGGAGAGTGAAGGAGGCGCTCGAGCAGCAG 735
 Qy 731 CACAGCGTCAGGTGGACACAGCTGCGATGCGAGGCGCAGAGCTGGAGGCGCGCTCCGC 790
 Db 736 CACAGCGTCAGGTGGACACAGCTGCGATGCGAGGCGCAGAGCTGGAGGCGCGCTCCGC 795
 Qy 791 ATGAGGCGCAGCGCGCTCGAGGAGAAAGAGAGTGGCCCAAGTTGAGGTGCGCTAT 850
 Db 796 ATGAGGCGCAGCGCGCTCGAGGAGAAAGAGAGTGGCCCAAGTTGAGGTGCGCTAT 855
 Qy 851 CACAGCTCTTCAAGAAATACGACCAACCATCAAGAGCAGCTGGTGGGAGGAGCGG 910
 Db 856 CACAGCTCTTCAAGAAATACGACCAACCATCAAGAGCAGCTGGTGGGAGGAGCGG 915
 Qy 911 AAGCGAGGAATGAGCTGGAAGATCTCAAAACAGCAGCTCCAGAGGCGCGAGAGCGCTG 970
 Db 916 AAGCGAGGAATGAGCTGGAAGATCTCAAAACAGCAGCTCCAGAGGCGCGAGAGCGCTG 975
 Qy 971 GTGGCCAAACAGAGGTGATCGATAAGCTGAAGAGGAGGCGGAGCAGCAAGATTGTG 1030
 Db 976 GTGGCCAAACAGAGGTGATCGATAAGCTGAAGAGGAGGCGGAGCAGCAGCAAGATTGTG 1035
 Qy 1031 ATGAGAGCGTTCGGGTGCTGAAGGCGCGGATATCTACAGGCGGAGCTTCCAGGCT 1090
 Db 1036 ATGAGAGCGTTCGGGTGCTGAAGGCGCGGATATCTACAGGCGGAGCTTCCAGGCT 1095
 Qy 1091 GAGAGCAGGCCCGGAGAGCTGGCCGAGAAAGAGAGTCTCTGAGGAGCAGCTGGAG 1150
 Db 1096 GAGAGCAGGCCCGGAGAGCTGGCCGAGAAAGAGAGTCTCTGAGGAGCAGCTGGAG 1155
 Qy 1151 CAGCTCAGAGGAGTACAGCAACTGAAGGCCAGCTGTGAGGAGTGGCCAGGATCGAG 1210
 Db 1156 CAGCTCAGAGGAGTACAGCAACTGAAGGCCAGCTGTGAGGAGTGGCCAGGATCGAG 1215


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QY 1211 GACATGAGGAAGCGGATGTCGAGGTCTCCAGGCCCCCTTGCCCCCGCCCTGCCTAC 1270
Db 1216 GACATGAGGAAGCGGATGTCGAGGTCTCCAGGCCCCCTTGCCCCCGCCCTGCCTAC 1275
QY 1271 CTCTCTCTCTCCCTGCGCCCTGCGCAGCAGAGGAGGAGGCCCCCGGAGGAGCCACTGAC 1330
Db 1276 CTCTCTCTCTCCCTGCGCCCTGCGCAGCAGAGGAGGAGGCCCCCGGAGGAGCCACTGAC 1335
QY 1331 TTCTGCTGTCCCAAGTGCAGTATCAGGCCCTGATATGACACCTGCGATACATATGTC 1390
Db 1336 TTCTGCTGTCCCAAGTGCAGTATCAGGCCCTGATATGACACCTGCGATACATATGTC 1395
QY 1391 ATGAGTGTGATTCAGTAGGCGCCGCGCAGTGCAGGCGCACTGCTGCGCCCGAGGAGCGGCC 1450
Db 1396 ATGAGTGTGATTCAGTAGGCGCCGCGCAGTGCAGGCGCACTGCTGCGCCCGAGGAGCGGCC 1454
QY 1451 GGGACCGTGCAGTCTGGCTTCTCTCTCCGCGCTGCTAGCCAGATGAAAGGGCTGGGT 1510
Db 1455 GGGACCGTGCAGTCTGGCTTCTCTCTCCGCGCTGCTAGCCAGATGAAAGGGCTGGGT 1514
QY 1511 GGCCACAACCTGGATGCCACTGAGGCCCCAGCCAGGAGCTGGCGGCGCACTTACGCT 1570
Db 1515 GGCCACAACCTGGATGCCACTGAGGCCCCAGCCAGGAGCTGGCGGCGCACTTACGCT 1574
QY 1571 TCAGCTGTGTA-TCCGCTGTGTCCTCTTTTGGGGTAGATGCGGCCCGCATCAGGCTGA 1629
Db 1575 TCAGCTGTGTA-TCCGCTGTGTCCTCTTTTGGGGTAGATGCGGCCCGCATCAGGCTGA 1634
QY 1630 CTCGCTGCTCTTTTGTCTCTCTCTCTGCTGCAACCACTTGCTCGGGCTAATCCCTC 1689
Db 1635 CTCGCTGCTCTTTTGTCTCTCTCTCTGCTGCAACCACTTGCTCGGGCTAATCCCTC 1694
QY 1690 CTTCTCTCCACCCGGCACTGGGAGTCAGAAATGGGGCTTGGGGCTCTCAGGGAGAA 1749
Db 1695 CTTCTCTCCACCCGGCACTGGGAGTCAGAAATGGGGCTTGGGGCTCTCAGGGAGAA 1754
QY 1750 CTGCTTCCCTTGGCAGAGCTGGGTGGCAGCTCTTCTCTCCACCGGACACCGACCCCGCG 1809
Db 1755 CTGCTTCCCTTGGCAGAGCTGGGTGGCAGCTCTTCTCTCCACCGGACACCGACCCCGCG 1814
QY 1810 CGCTGTGCTGGGAGTGTGCGCTCTTACATGACACCGGCTGTCTCTCTTTGGGCT 1869
Db 1815 CTGCTGTGCTGGGAGTGTGCGCTCTTACATGACACCGGCTGTCTCTCTTTGGGCT 1874
QY 1870 GCATGCTATTCCATTTTGACGACAGCCGATGTATTTAAACAGTCACTATTGATGAC 1929
Db 1875 GCATGCTATTCCATTTTGACGACAGCCGATGTATTTAAACAGTCACTATTGATGAC 1934
QY 1930 ATTTGGGTTGTTCCCATCTTTTGTACCAATAATAATGGCATAGTAAAAA 1982
Db 1935 ATTTGGGTTGTTCCCATCTTTTGTACCAATAATAATGGCATAGTAAAAA 1987
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RESULT 8
US-10-761-370-2
; Sequence 2, Application US/10761370
; Publication No. US20040219615A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR
; FILE REFERENCE: WALLACH=27
; CURRENT APPLICATION NUMBER: US/10/761,370
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: US/09/646,403
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: IL 123758
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: PCT/IL99/00158
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: IL 126024
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; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-761-370-2
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Query Match 88.1%; Score 1757.2; DB 18; Length 2034;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1826; Conservative 3; Mismatches 21; Indels 8; Gaps 5;

QY 132 AGCCCTTGCCCTTGTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGTGC 191
Db 155 AGCCCTTGCCCTTGTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGTGC 214
QY 192 AGCCCAAGTGGTGGCCCGGCGAGCAGATCAGGACGTACTGGGGCGAAGAGTCTCTCTGGGGA 251
Db 215 AGCCCAAGTGGTGGCCCGGCGAGCAGATCAGGACGTACTGGGGCGAAGAGTCTCTCTGGGGA 274
QY 252 AGCCAGCCATGCTGCACCTGCTTCAGAAACAGGGGCGCTCTGAGACCTCTCAGCGCTGCC 311
Db 275 AGCCAGCCATGCTGCACCTGCTTCAGAAACAGGGGCGCTCTGAGACCTCTCAGCGCTGCC 334
QY 312 T-GGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGSCAG-AGCAACCAGATTCTGCGGGA 369
Db 335 TGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGSCAGTAGCAACACGATTCTTGGGG 394
QY 370 GCGCTGCGAGAGCTTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 425
Db 395 AGCTGCGGAGGAGGAGCTTTCTGCAATTTTCTCAAGCCAGCCAGAGGGAGGAGGAGTTC 454
QY 426 TCATGTGCAAGTTTCAGAGGAGGCGCAGGAACTGGTGGAGAGACTCGGCCCTGGAGAACTCG 485
Db 455 TCATGTGCAAGTTTCAGAGGAGGCGCAGGAACTGGTGGAGAGACTCGGCCCTGGAGAACTCG 514
QY 486 ATCTGAAGAGGCGAGAGGAGCAGGCTCTCGCGGAGGTGGAGCACCTGAAAGAGATGCCAGC 545
Db 515 ATCTGAAGAGGCGAGAGGAGCAGGCTCTCGCGGAGGTGGAGCACCTGAAAGAGATGCCAGC 574
QY 546 AGCAGATGCTCTGAGGACAAAGGCTCTGTGAAAGCCAGGTGACGTCTTTGCTCGGGGAGC 605
Db 575 AGCAGATGCTCTGAGGACAAAGGCTCTGTGAAAGCCAGGTGACGTCTTTGCTCGGGGAGC 634
QY 606 TGCAGAGAGCCAGAGTGTGAGGCTGCGCACTAAGGAATGCCAGGCTCTGAGAGGCTC 665
Db 635 TGCAGAGAGCCAGAGTGTGAGGCTGCGCACTAAGGAATGCCAGGCTCTGAGAGGCTC 694
QY 666 GGGCCCGGCGCCAGCAGCAGGCGCGCAGCTGGAGAGTGGCGGCGGAGGCGCTGCAGC 725
Db 695 GGGCCCGGCGCGCCAGCAGCAGGCGCGCAGCTGGAGAGTGGCGGCGGAGGCGCTGCAGC 754
QY 726 AGCAGCACAGCGTGCAGGTGGACCAAGCTGCGCATGCGGGCCAGAGCGCTGGAGGCGCGC 785
Db 755 AGCAGCACAGCGTGCAGGTGGACCAAGCTGCGCATGCGGGCCAGAGCGCTGGAGGCGCGC 814
QY 786 TCCGATGAGGCGCAGCGCGCTCGAGGAGAAAGGAAGCTGGCCCAAGTTGAGGTGG 845
Db 815 TCCGATGAGGCGCAGCGCGCTCGAGGAGAAAGGAAGCTGGCCCAAGTTGAGGTGG 874
QY 846 CCTATCACCAGCTCTTCAAGAAATACGACCAACCATCAAGAGACGCTGGTGGGCGAGTG 905
Db 875 CCTATCACCAGCTCTTCAAGAAATACGACCAACCATCAAGAGACGCTGGTGGGCGAGTG 934
QY 906 AGCGGAAGCGAGAAATGCAAGTGGAGATCTCAAAACAGCAGCTCCAGCAGGCGCGAGGAG 965
Db 935 AGCGGAAGCGAGAAATGCAAGTGGAGATCTCAAAACAGCAGCTCCAGCAGGCGCGAGGAG 994
QY 966 CCTGTGTGCGCAACAGGAGGTGATCGATAGCTGAAAGAGGAGGCGCGAGCAGCAAGA 1025
Db 995 CCTGTGTGCGCAACAGGAGGTGATCGATAGCTGAAAGAGGAGGCGCGAGCAGCAAGA 1054
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QY	1026	TTGTGATGGAGACCGTTCCCGTGTCTGAAGCGCCGAGCGGATATCTACAAGCGGACTTCC	1085
Db	1055	TTGTGATGGAGACCGTTCCCGTGTCTGAAGCGCCGAGCGGATATCTACAAGCGGACTTCC	1114
QY	1086	AGGCTTGAGAGGCGAGGCCCGGAGAAAGCTGGCCGAGAAAGAGAGCTCTCTGCAGGAGCAGC	1145
Db	1115	AGGCTTGAGAGGCGAGGCCCGGAGAAAGCTGGCCGAGAAAGAGAGCTCTCTGCAGGAGCAGC	1174
QY	1146	TGGAGCAGCTGCAGAGGGAGTACAGCAAACTGAAGGCCAGCTGTCTCGAGTTCGGCCAGGA	1205
Db	1175	TGGAGCAGCTGCAGAGGGAGTACAGCAAACTGAAGGCCAGCTGTCTCGAGTTCGGCCAGGA	1234
QY	1206	TCGAGGACATAGAGGAGCGGATGTTCGAGTCTTCCAGGCCCTCTTGGCCCCCCTCGCTG	1265
Db	1235	TCGAGGACATAGAGGAGCGGATGTTCGAGTCTTCCAGGCCCTCTTGGCCCCCCTCGCTG	1294
QY	1266	CCTACTCTCTCTTCCCTTGGCCCTGCCAGCAGAGAGAGAGCCCCCCGAGAGAGCAC	1325
Db	1295	CCTACTCTCTCTCTTCCCTTGGCCCTGCCAGCAGAGAGAGAGCCCCCCGAGAGAGCAC	1354
QY	1326	CTGACTTCTGCTGCCAAAGTGGCAGTATTACAGGCCCTGTATATGACACACCTTCAGATAC	1385
Db	1355	CTGACTTCTGCTGCCAAAGTGGCAGTATTACAGGCCCTGTATATGACACACCTTCAGATAC	1414
QY	1386	ATGTCATGGAGTGCAATTGATGAGGCCGGCCAGTGCAGGCCACTTCGTGCTGCCAGGACG	1445
Db	1415	ATGTCATGGAGTGCAATTGATGAGGCCGGCCAGTGCAGGCCACTTCGTGCTGCCAGGACG	1473
QY	1446	TGCCCGGAGCCGTCGACGCTGCGCTTTCCTTCCCGCCTGCTAGCCAGGATGAAAGGC	1505
Db	1474	TGCCCGGAGCCGTCGACGCTGCGCTTTCCTTCCCGCCTGCTAGCCAGGATGAAAGGC	1533
QY	1506	TGGGTGGCCACAACCTGGGATGCCACCTGGAGGCCACCCAGAGAGTGGCCCGCGCACCTT	1565
Db	1534	TGGGTGGCCACAACCTGGGATGCCACCTGGAGGCCACCCAGAGAGTGGCCCGCGCACCTT	1593
QY	1566	AGCCTTCAGCTGTTGA--TCGCGTGGTCCCTCTTTTGGGGTAGATGCGGCCCGGATCAGG	1624
Db	1594	AGCCTTCAGCTGTTGATTTCGCGTGGTCCCTCTCTTTTGGGGTAGATGCGGCCCGGATCAGG	1653
QY	1625	CCTGACTCGCTGCTCTTTTGTTCCTCTGTCTGCTCGAACCACTGGCTCGGGGCTTAAT	1684
Db	1654	CCTGACTCGCTGCTCTTTTGTTCCTCTGTCTGCTCGAACCACTGGCTCGGGGCTTAAT	1713
QY	1685	CCCTCCCTCTTCTTCCACCCGGCACTGGGGGAAGTCAAGAAATGGGGCTCTGGGGCTCTCAGG	1744
Db	1714	CCCTCCCTCTTCTTCCACCCGGCACTGGGGGAAGTCAAGAAATGGGGCTCTGGGGCTCTCAGG	1773
QY	1745	GAGAACTGCTTCCCTCGGAGAGCTGGGTGGGAGCTCTTCTCTCCACCGGACACCGACCC	1804
Db	1774	GAGAACTGCTTCCCTCGGAGAGCTGGGTGGGAGCTCTTCTCTCCACCGGACACCGACCC	1833
QY	1805	GCCCGCGCTGTGGCCCTGGGAGTGTCGCCCTCTTACCATGACACAGGGTGCTCTCCTTTT	1864
Db	1834	GCCCGCTGCTGTGGCCCTGGGAGTGTCGCCCTCTTACCATGACACAGGGTGCTCTCCTTTT	1893
QY	1865	GGGCTGCAATGCTATTCCTATTTGCAGCCAGACCGATGTGTATTAAACAGTCACTATTGA	1924
Db	1894	GGGCTGCAATGCTATTCCTATTTGCAGCCAGACCGATGTGTATTAAACAGTCACTATTGA	1953
QY	1925	TGGACATTTGGGTGTTTCCATCTTTTGTGTACATAAATAATGGCATAGTAAAAA	1982
Db	1954	TGGACATTTGGGTGTTTCCATCTTTTGTGTACATAAATAATGGCATAGTAAAAA	2011

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; TITLE OF INVENTION: IKKKG
; FILE REFERENCE: R03-011-208PV
; CURRENT APPLICATION NUMBER: US/10/792,063
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 06/452,293
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-063-4

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RESULT 9

US-10-792-063-4
; Sequence 4, Application US/10792063
; Publication No. US2004017579A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jason
; APPLICANT: Garrett-Engle, Phillip
; APPLICANT: Kan, Zhengyan

QY 1511 GGCCAACTGGGATGCCACCTGGAG 1536
Db 1430 TTAGCCCTTTGGTCCCAATTTAGG 1455

RESULT 11
US-10-408-305-2
; Sequence 2, Application US/10408305
; Publication No. US20030228667A1
; GENERAL INFORMATION:
; APPLICANT: SHOJI, YAMAOKA
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE ENCODING A MODULATOR OF NF-KB
; FILE REFERENCE: 0660-0146-55
; CURRENT APPLICATION NUMBER: US/10/408,305
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US/09/253,701
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1874
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-408-305-2

Query Match 47.2%; Score 940.4; DB 17; Length 1874;
Best Local Similarity 80.7%; Pred No. 3e-243;
Matches 1134; Conservative 0; Mismatches 246; Indels 26; Gaps 2;

QY 131 CAGCCCTTGCCCTGTGTGAATAGGCACTCTGGAAGACCCAACTGTGTGATGGTG 190
Db 76 CAGACACTGTCTGTGTGATGAACAAGCAACCCCTTGGAAACCACTGAGTGAGACGGTG 135

QY 191 CAGCCAGTGTGGCCCGCAGCAGATCAGACGCTACTGGCGGAAGAGTCTCTCTGGGG 250
Db 136 CAGCCAGTGTGGCCCGCAGCAGACCAACATCTGTGGGTGAAGATCTCTCTGGGG 195

QY 251 AAGCCAGCATGCTGCACCTGCTTCAAGACAGGCGCTCTGAGACCCCTCCAGCGCTGC 310
Db 196 AAGCTGTCAATGCTACATCTGCTTCAGACAGGGTACTCTGAGACCTCCAGCGCTGC 255

QY 311 CTGGAGGAGATCAAGAGCTCGAGATGCCATCCGCGAGACCAACAGATTTCTCGGGAG 370
Db 256 CTGGAGGAGATCAAGAGCTCGAGATGCCATCCGCGAGACCAACAGATTTCTCGGGAG 315

QY 371 CGCTCGAGGAGCTTCTGCATTTCCAGACCCAGAGGAGGAGAGAGTTCCTCATG 430
Db 316 CGCTGTGAGAGCTGCTGCATTTCCAGTCAAGTCAAGCAGCGGAGGAGAGTTCCTTATG 375

QY 431 TGCAGATTCAGAGGAGCCAGGAACTGGTGGAGAGACTCGGCCCTGGAGAAAGCTCGATCTG 490
Db 376 TGCAGATTCAGAGGAGCCAGGAACTGGTGGAGAGACTCGGCCCTGGAGAAAGCTCGATCTG 435

QY 491 AAGAGGCAAGAGGAGCAGGCTCTCGGGAGGTGAGCAGCACTGAAGATGCCAGCAGCAG 550
Db 436 CAGAGTCAAGAGGAGCAGGCTTTAAGAGGTGAGCAACTGAAGAAATGCCAACAGCAG 495

QY 551 ATGGCTGAGGACAAGGCTCTGTGAAAGCCAGGTGACCTCTTGTCTCGGGAGCTGCAG 610
Db 496 ATGGCTGAGGACAAGGCTCTGTGAAAGCTGAGTGACATCTTGTCTCGGAGAACTCCAG 555

QY 611 GAGAGCCAGATCGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGGTCCGGCC 670
Db 556 GAGAGCCAGAGCCGTTTGGAGGCTGCCCAAGGATCGCAAGCTTTAGAGGGAAGGATT 615

QY 671 CGGGCGCCAGCAGGAGCGCGCAGCTGGAGATGAGCGCAGCGCTGAGCAGCAGCAG 730
Db 616 CGAGCAGTATGAGCAGGTCAGACACTGGAGATGAGCGGAGGTGCTTACAGCAGCAG 675

QY 731 CACAGCTGCAAGTGGACCACTCGCATGCAAGGCGCAGAGCGTGGAGGCGCGGCTCCGC 790
Db 676 CACAGCGTCCAGGTGGACCACTGCGTATGACAGACCAAGAGCGTGGAGGCTGCTTGGCA 735

QY 791 ATGAGCGCCAGCGCCGCTCGAGGAGAAAGAGAGCTGGCCCACTTGCAGGTGCGCTAT 850
Db 736 ATGAGCGCGCAGGCTGCTTCAGAGGAGAAAGGAGCTGGCTCAGTTGCAGGACGCTAT 795

QY 851 CACCAGCTCTTCCAAGATACGCAACACATCAAGAGCAGCGTGTGGGCGAGTGGCGG 910
Db 796 CACCACTCTTCCAGACTACGACAGCCACATTAAGAGCAGCAAG-----840

QY 911 AAGCGAGAAATGCAAGCTGGAAGATCTCAACAGCAGCTCCAGAGGCGCCAGAGCCCTG 970
Db 841 -----GGCATGCACTGGAAGATCTGAGGCAACAGCTCCAGAGCTGAGAGGCCCTG 894

QY 971 GTGGCCAAACAGAGGATGATCGATAAGCTGAAGAGAGGCGGAGCAGACAAAGATTGTG 1030
Db 895 GTAGCCAAACAGGAATTTGATTAACTGAAGAGGAGGCTGAGCAGCACAAGATTGTG 954

QY 1031 ATGGAGACCTTCCGGTCTGAAAGGCCAGCGCATATCTAACAAGGCGGACTTCCAGGCT 1090
Db 955 ATGGAGACTGTGCCAGTCTTGAAGGCCAGCGGATATCTAACAAGGCTGACTTCCAAGCT 1014

QY 1091 GAGAGCAGGCCCGGAGAAAGCTGGCCGAGAAAGAGAGTCTCTGAGAGCAGCTGGAG 1150
Db 1015 GAGAGGCAATGCCCGGAGAAAGCTGGTGCAGAAAGAGAGTATTTGCAAGGAGCAGCTGGAG 1074

QY 1151 CAGCTGCAAGGAGTACAGCAAACTGAAGGCCAGCTGTCAAGAGTCCGCCAGGATCGAG 1210
Db 1075 CAGCTGCAAGGAGTACAGCAAACTGAAGGCCAGCTGTCAAGAGTCCGCCAGGATCGAG 1134

QY 1211 GACATGAGGAGGCGCATGTGAGAGTCTCCAGGCGCCCTTGGCCCGCCCTGCGCTAC 1270
Db 1135 GATATGAGGAGGCGCATGTAGAGACTCCCGCGCTCTTTACTCTCTGCTCCAGCTCAC 1194

QY 1271 CTCTCTCTCTCTGCGCCCTGCGCCAGCAGAGAGAGGCGCCCGAGGAGCAGCAGCTGAC 1330
Db 1195 CACTCTCTCTCTGCGCCCTGCGCCAGCAGAGAGGAGGCGCTCTCTGAAGAACCTCTGAC 1254

QY 1331 TTCTGTGTGTCAGAGTCCAGTATCAGGCGCTGATATGACACCTTGCAGATACATGTC 1390
Db 1255 TTCTGTGTGTCAGAGTCCAGTATCAGGCTCTGATATGACACTCTACAGATACATGTC 1314

QY 1391 ATGAGTGTGATGATGAGGCGCCAGTGCAGAGGCGCACTGCGCTGCGCCAGGAGCTGCC 1450
Db 1315 ATGAGTGTGATGATGAGGCGCCAGTGCAGAGGCGCACTGCGCTGCGCTGCGCTGCGCT 1369

QY 1451 GGGACGCTGAGTCTGCGCTTCTCTCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 1510
Db 1370 TGATCTGTGATGCTGCTTCTCTCTGCTTTTACCTGATAGTCCACACTTAAGGCTTGT 1429

QY 1511 GGCCAACTGGGATGCCACCTGGAG 1536
Db 1430 TTAGCCCTTTGGTCCCAATTTAGG 1455

RESULT 12

US-09-863-049A-1

; Sequence 1, Application US/09863049A

; Publication No. US20030032055A1

; GENERAL INFORMATION:

; APPLICANT: Kenrick, Sue J.

; APPLICANT: Nelson, David L.

; APPLICANT: Aradhya, Swaroop

; APPLICANT: D'Urso, Michele

; APPLICANT: Woffendin, Hayley

; APPLICANT: Munnich, Arnold

; APPLICANT: Smahl, Asmaa

; APPLICANT: Israel, Alain

; APPLICANT: Poustka, Annemarie

; APPLICANT: Lewis, Richard A

; APPLICANT: Levy, Moise

; APPLICANT: Heiss, Nina

; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Defe

; TITLE OF INVENTION: NPKAPPA B (NF-KB) Activation

; FILE REFERENCE: HO-P01961US1


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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-063-6

Query Match      20.2%; Score 402.6; DB 18; Length 483;
Best Local Similarity 99.0%; Pred. No. 3.1e-98;
Matches 405; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 149 ATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGTGCAGCCAGTGGTGGCCG 208
Db 1 ATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGTGCAGCCAGTGGTGGCCG 60

Qy 209 GCAGCAGATCAGGACGTACTTGGCGGAAGAGTCTCTCTGGGGAAGCCAGCCATGTGCAC 268
Db 61 GCAGCAGATCAGGACGTACTTGGCGGAAGAGTCTCTCTGGGGAAGCCAGCCATGTGCAC 120

Qy 269 CTGCTTTCAGACAGGCGCTCTCTGAGACCTTCCAGCCCTCCAGCGCTGGAGGAGAAATCAAGAG 328
Db 121 CTGCTTTCAGACAGGCGCTCTCTGAGACCTTCCAGCCCTCCAGCGCTGGAGGAGAAATCAAGAG 180

Qy 329 CTCGAGATGCCATCCGGCAGAGCAACAGATTCTCGCGGAGCGCTGCGAGGAGCTTCTG 388
Db 181 CTCGAGATGCCATCCGGCAGAGCAACAGATTCTCGCGGAGCGCTGCGAGGAGCTTCTG 240

Qy 389 CATTTCCAGCCAGCCAGAGGAGAGAGAGAGTTCCTCATGTGCAAGTTCAGGAGGCC 448
Db 241 CATTTCCAGCCAGCCAGAGGAGAGAGAGAGTTCCTCATGTGCAAGTTCAGGAGGCC 300

Qy 449 AGGAACTCGTGGAGAGACTCGGCTGGAGAGCTCGATCTGAAGAGCCAGAGGAGCAG 508
Db 301 AGGAACTCGTGGAGAGACTCGGCTGGAGAGCTCGATCTGAAGAGCCAGAGGAGCAG 360

Qy 509 GCTCTCGGGAGGTGGAGCCTGAAGAGATGCCAGCAGCAGATGGCTG 557
Db 361 GCTCTCGGGAGGTGGAGCCTGAAGAGATGCCAGCAGCAGAGGAGCTG 409
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RESULT 15

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US-09-925-298-84/c
; Sequence 84, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 2803
; TYPE: DNA
; ORGANISM: Homo sapiens
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; LOCATION: (10)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (517)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (572)
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US-09-925-298-84
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Best Local Similarity 95.2%; Pred. No. 3.1e-64;
Matches 280; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

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Qy 251 AAGCCAGCCATGTGTGCACTTGGCTTTCAGAACAGGGCGCTCTGTGAGACCTCCAGCGCTGC 310
Db 182 AAGCCAGCCATGTGTGCACTTGGCTTTCAGAACAGGGCGCTCTGTGAGACCTCCAGCGCTGC 123

Qy 311 CTGAGGAGAGATCAAGAGCTCCGAGATGCCATCCGCGAGGAGCAACCAAGTTCGCGGGAG 370
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Qy 371 CGTTCGAGGAGCTTCTGCAATTTCCAAAGCCAGCCAGAGGAGGAGAGAGTTC 424
Db 62 CGTTCGAGGAGCTTCTGCAATTTCCAAAGCCAGCCAGAGGAGGAGAGAGTTC 9
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Search completed: February 9, 2005, 03:17:38
Job time : 1093 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 21:27:04 ; Search time 6675 Seconds
(without alignments)
11370.809 Million cell updates/sec

Title: US-09-377-795-1

Perfect score: 1994

Sequence: 1 ggcagcagatggccctgt.....gtataaaaaaaaaaaaaa 1994

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1820.4	91.3	1958	3	CR600010 full-leng
3	1816.8	91.1	1962	6	CA916723 K142FL hu
4	1794.4	90.0	1943	3	CR604149 full-leng
5	1466.4	73.5	1751	3	CR603029 full-leng
6	1151.4	57.7	1164	3	CR612085 full-leng
C 7	997.4	50.0	1039	1	AL575675 full-leng
C 8	948	47.5	1115	1	AL582339 full-leng
C 9	927.6	46.5	4335	3	AK037020 Mus muscu
C 10	916.8	46.0	1081	1	AL568758 full-leng
C 11	914.2	45.8	1036	5	BC325315 full-leng
C 12	880.2	44.1	1118	5	BC332283 full-leng
C 13	877.6	44.0	908	5	BQ674261 full-leng
C 14	866.6	43.5	913	1	AL572134 full-leng
C 15	859.2	43.1	935	1	AL580495 full-leng
C 16	850	42.6	888	1	AL521144 full-leng
C 17	834.2	41.8	1016	5	EX361771 full-leng
C 18	828.8	41.6	879	5	BC351837 full-leng
C 19	824.8	41.4	925	5	BC328265 full-leng
C 20	822.2	41.2	1043	1	AL541141 full-leng
C 21	818.8	41.1	974	1	AL545822 full-leng
C 22	813.6	40.8	878	5	BUI97200 full-leng
C 23	813	40.8	875	1	AL558739 full-leng
C 24	809.8	40.6	975	5	BC418245 full-leng

25	802.6	40.3	833	5	BQ439256	BQ439256	AGENCOURT
26	778.8	39.1	1011	5	BC325316	BC325316	AGENCOURT
27	778.8	39.1	1098	4	BM473416	BM473416	AGENCOURT
28	774.8	38.9	957	5	BQ932422	BQ932422	AGENCOURT
29	765	38.4	1024	1	AL558226	AL558226	AGENCOURT
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C 31	762.2	38.2	974	1	AL562815	AL562815	AGENCOURT
C 32	761	38.2	919	1	AL547021	AL547021	AGENCOURT
C 33	754.6	37.8	920	5	BC418246	BC418246	AGENCOURT
C 34	742.6	37.2	858	1	AL571390	AL571390	AGENCOURT
C 35	739.8	37.1	902	5	BQ944161	BQ944161	AGENCOURT
C 36	738.4	37.0	872	5	BC418606	BC418606	AGENCOURT
C 37	732.6	36.7	865	5	BUI70415	BUI70415	AGENCOURT
C 38	712.6	35.7	1091	4	BM467195	BM467195	AGENCOURT
C 39	702	35.2	877	5	BC434638	BC434638	AGENCOURT
C 40	697.8	35.0	931	5	BUI54734	BUI54734	AGENCOURT
C 41	693.4	34.8	707	5	BUI616100	BUI616100	AGENCOURT
C 42	688.4	34.5	701	5	BUI626925	BUI626925	AGENCOURT
C 43	688.4	34.5	701	5	BUI633401	BUI633401	AGENCOURT
C 44	685.6	34.4	929	5	BUI528711	BUI528711	AGENCOURT
C 45	683.6	34.3	708	5	BUI5463	BUI5463	AGENCOURT

ALIGNMENTS

BC046922 1960 bp mRNA linear HTC 19-NOV-2003
Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma, mRNA (cdna clone IMAGE:5476394), containing frame-shift errors.

BC046922 GI:28422142

HTC.

Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

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Homo sapiens

Homo sapiens

Homo sapiens

Craniata: Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1960)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
23388257
MEDLINE
PUBMED
12477932
2 (bases 1 to 1960)
Straussberg, R.
Direct Submission
Submitted (14-FEB-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs@mail.nih.gov

Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Contact: nisc.mgc@nih.gov
Web site: <http://www.nisc.nih.gov/>
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Scantripp, S., Thomas, P.J., Touchman, J.W.,
Tsurgoun, C., Vogt, J.B., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Query Match	92.8%;	Score 1850.4;	DB 3;	Length 1960;
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Db 1865 CATGCTATTCCATTTTGCAGCAGACCGATGTTATTTAAACAGTCACTATTGATGACA 1924
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RESULT 3
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LOCUS
DEFINITION
CA916723 human keratinocyte matchmaker cDNA library Homo sapiens cDNA
clone K142 5' similar to IKK gamma/ NEMO, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1962)
Scarfia, L.E., Stouffer, S.D. and Swinney, D.C.
Identification of Ring Finger proteins that interact with Ubch5a,
an ubiquitin-conjugating enzyme
Unpublished (2002)
Contact: Scarfia LE
Enzymology
Roche Bioscience
3401 Hillview Ave, S3-1, Palo Alto, CA 94304-1397, USA
Tel: 650 354 7997
Fax: 650 354 7554
Email: liliana.scarfia@roche.com
Full length single stranded sequencing of baited insert
Insert Length: 2000 Std Error: 0.00
Seq primer: primer 2 (5395)TACCACATCAATGGATG; and insert-specific
POLYA=Yes.

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/lab_host="yeast/E.coli"
/clone_lib="human keratinocyte matchmaker cDNA library"
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Matchmaker yeast two-hybrid system from Clontech; pACT2
vector has GAL4 AD and HA epitope under ADH1 promoter.
This oligo-dT primed library was screened with human
Ubch5a as bait, to obtained interacting proteins."
ORIGIN
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Best Local Similarity 99.6%; Pred. No. 0;
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Db 288 CTGAGGAGAACTCAAGAGCTCCGAGATGCCATCCGCGAGAGCAACAGATTTCTCGGGAG 347
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Db 348 CGCTGCGAGAGCTTCTGCAATTTTCAAGCCAGCCAGAGGAGGAGAGAGTTCCTCATG 407
QY 431 TGCAAGTTTCAGGAGGCGCAGGAACTGTTGAGAGACTCGGCCCTGGAGAGCTCGATCTG 490
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QY 491 AAGAGCAGAGAGAGAGCTCTGCGGAGAGTGGAGCACTTGAAGAGATGCCAGCAGCAG 550
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1019 TGTGATGGAGACGCTTCCGCTGCTGAAGCCAGCGGATATCTCAAGCGGAGCTTCCA 1078
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Db 1678 CTCCTCTTCTCCACCGGCACTGGGGAAGTCAAGAAATGGGCTTGGGCTCTCAGGGA 1737
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Db 1738 GAACTGCTTCCCTCGGAGAGCTGGGTGGAGCTTCTCTCCACCGGACACCGCCCGC 1797
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Qy 1867 GCTCATGCTATTCATTTTCAGCAGCAGACCGAGTGTATTTAACAGTCACTATTGATG 1926
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Qy 1927 GACATTTGGGTGTTTCCATCTTTT 1952
Db 1918 GACATTTGGGTGTTTCCCATCTTTT 1943

RESULT 5
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LOCUS full-length cDNA clone CS0DC017YA10 of Neuroblastoma Cot
DEFINITION 25-normalized of Homo sapiens (human).
ACCESSION CR603029
VERSION CR603029.1 GI:50483836
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1751)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 1751)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen.
FEATURES
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Query Match 73.5%; Score 1466.4; DB 3; Length 1751;
Best Local Similarity 91.4%; Pred. No. 1.9e-302;
Matches 1641; Conservative 0; Mismatches 1; Indels 154; Gaps 2;
Qy 131 CAGCCCTTGGCTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGT 190
Db 110 CAGCCCTTGGCTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGT 169
Qy 191 CAGCCAGTGGTGGCGCGGAGCAGAGTCAAGAGCTACTGGCGGAGAGTCTCTCTGGGG 250
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[illegible]

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Qy	1391	ATGAGTGCATTTAGTAGG	CGCGCCAGTGC	CAAGGCCACTGCTTGC	1450
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Qy	1451	GGGACCGTGCAGTCTGG	CTTTCCTTCCCGCTGCTAG	CCACGAGTGAAGGGCTGGGT	1510
Db	1276	GGGACCGTGCAGTCTGG	CTTTCCTTCCCGCTGCTAG	CCACGAGTGAAGGGCTGGGT	1335
Qy	1511	GGCCACAATCGGATGCA	CTGAGAGCCCAACGAGAGCT	TGCGCGGCGACCTTACGCT	1570
Db	1336	GGCCACAATCGGATGCA	CTGAGAGCCCAACGAGAGCT	TGCGCGGCGACCTTACGCT	1395
Qy	1571	TCAGCTGTTGATCCGCT	GTGTCCTCTTTTGGGGTAGAT	TGCGGCCCGGATCAGGCGCTGAC	1630
Db	1396	TCAGCTGTTGATCCGCT	GTGTCCTCTTTTGGGGTAGAT	TGCGGCCCGGATCAGGCGCTGAC	1455
Qy	1631	TGCGTGTCTTTTGTGTC	TGCTGCTGCTGCTGCA	ACCACTTGGCTGGGCTAATCCCTCC	1690
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Qy	1691	CTCTTCTCCACCGGAC	TGGGGAAGTCAAGAAATGG	GGGCTCGGGGCTCTCAGGAGAAC	1750
Db	1516	CTCTTCTCCACCGGAC	TGGGGAAGTCAAGAAATGG	GGGCTCGGGGCTCTCAGGAGAAC	1575
Qy	1751	TGCTTCTCCCTGGCAG	AGCTGGGTGGCAGCTCTT	TCCTCCCAACCGGACACCGCCGCGC	1810
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Qy	1811	CGCTGTGCCCTGGAG	TGTCGCCCTCTTACCATGC	ACAGGGTGCTCTCTTTTGGGCTG	1870
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Qy	1871	CATGCTATTCCATTTT	GCAGCCAGACCGATGTG	TATTTAACCAAGTCACTATTTCATG	1926
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RESULT 6					
LOCUS	CR612085		1164 bp	mRNA	linear HTC 21-JUL-2004
DEFINITION	Full-length cDNA clone CS0D0015F17 of T cells (Jurkat cell line)				
	Cot 10-normalized of Homo sapiens (human).				
ACCESSION	CR612085				
VERSION	CR612085.1	GI:50492892			
KEYWORDS	HTC; CNSLIT_cDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1164)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Paraday Avenue				
REFERENCE	2 (bases 1 to 1164)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				

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Best Local Similarity		99.8%;	Pred. No. 3.6e-235;
Matches 1163;		Conservative	0; Mismatches 1; Indels 1; Gaps 1;
QY	799	CCAGGCGCGCTCGAGGAGAGGAGGAGCTGGCCCGAGTTGCGAGTGGCGCTATCACAGCT	858
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QY	859	CTTCCAAAGATACGACACACATCAAGAGCAGCGTGGTGGCAGTGAGCGGAAGCGAGG	918
Db	61	CTTCCAAAGATACGACACACATCAAGAGCAGCGTGGTGGCAGTGAGCGGAAGCGAGG	120
QY	919	AATGCAAGTGAAGATCTCAACAGCAGCTTCAGCAGGCGGAGGCGGCTGGTGGCCAA	978
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QY	979	ACAGGAGGTGATCGATAGCTGAGGAGGAGCGGAGGAGCGACGACGATGATGAGGAG	1038
Db	181	ACAGGAGGTGATCGATAGCTGAGGAGGAGCGGAGGAGCGACGACGATGATGAGGAG	240
QY	1039	CGTTCCGGTGTCAAGCGCCAGCGGATATCTACAGGCGGACTTCCAGGCTGAGAGCA	1098
Db	241	CGTTCCGGTGTCAAGCGCCAGCGGATATCTACAGGCGGACTTCCAGGCTGAGAGCA	300
QY	1099	GGCCCGGAGAACTGGCCGAGAGGAGGAGTCTTCAGGAGCAGCTGGAGCAGCTGCA	1158
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QY	1459	GCAGTCTGGCTTCTCTCCGCGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1518
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QY	1579	TGATCGCTGGTCCCTCTTTTGGGTTAGTACGCGCCCGGATCAGGCGCTGATCGCTGCT	1638
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QY	1639	CTTTTGTTCCTTCTGTCTGCTCAACACTTGTGCTGGGCTAATCCCTCCCTCTTCTCT	1698
Db			

Db	840	CTTTTGTTCCTCTGCTCTGCTCGAACACATTTGGCCTCGGGCTAAATCCCTCCTCCCTCTTCTCT	899
QY	1699	CCACCCGGCACTGGGGAAGTCAAGAAATGGGGCTCTGGGGCTCTCAGGAGAACTGCTTCCC	1758
Db	900	CCACCCGGCACTGGGGAAGTCAAGAAATGGGGCTCTGGGGCTCTCAGGAGAACTGCTTCCC	959
QY	1759	CTGGCAGAGCTGGGTGGCAGCTCTTCTCTCCACCGGACACCGACCCGCGCGCTGTGC	1818
Db	960	CTGGCAGAGCTGGGTGGCAGCTCTTCTCTCCACCGGACACCGACCCGCGCGCTGTGC	1019
QY	1819	CCTGGAGTGTGCTCTTACCATGACACGGGTGCTCTCTTTTGGGCTGCATGCTAT	1878
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QY	1879	TCCATTTTGCAGCAGCAGCGATGTGTTTAAACCACTTATTTGATGGACATTTGGGTT	1938
Db	1080	TCCATTTTGCAGCAGCAGCGATGTGTTTAAACCACTTATTTGATGGACATTTGGGTT	1139
QY	1939	GTTTCCCATCTTTTGTGTACCATTA	1963
Db	1140	GTTTCCCATCTTTTGTGTACCATTA	1164
RESULT 7			
AL575675/c			
LOCUS			
DEFINITION			
AL575675 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA			
clone CS0D1069YK01 3-PRIME, mRNA sequence.			
ACCESSION			
AL575675			
VERSION			
AL575675.3 GI:46248619			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
REFERENCE			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS			
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
TITLE			
Full-length cDNA libraries and normalization			
JOURNAL			
Unpublished (2001)			
COMMENT			
On Feb 16, 2001 this sequence version replaced gi:31313981.			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
end enriched, double-strand cDNA was digested with Not I and cloned			
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library			
was normalized. Library was constructed by Life Technologies, a			
division of Invitrogen. This sequence belongs to sequence cluster			
10873.f			
For more information about this cluster, see			
http://www.genoscope.cns.fr/cdna?s=CS0D1069AF01NP1&c=10873.f.			
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		primer. Five prime end enriched, double-strand cDNA was	
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		sites of the pCMVSPORT 6 vector. Library was normalized."	
ORIGIN			
Query Match		50.0%;	Score 997.4; DB 1; Length 1039;
Best Local Similarity		98.8%;	Pred. No. 2.8e-202;
Matches 1023;		Conservative	2; Mismatches 8; Indels 2; Gaps 2;
QY	929	GAAGATCTCAACAGCAGCTCCAGCAGGCGGAGGAGGCGCTGGTGGCCAAACAGGAGGTG	988
Db	1034	GAAGATCTCAACAGCAGCTCCAGCAGGCGGAGGAGGCGCTGGTGGCCAAACAGGAGGTG	975

Qy	989	ATCGATAAGCTGAAGAGGAGGCGCGAGCAGCAAGAATTGTGATGGAGAACCGTTCCGGTG	1048
Db	974	ATCGATAAGCTGAAGAGGAGGCGCGAGCAGCAAGAATTGTGATGGAGAACCGTTCCGGTG	916
Qy	1049	CTGAAGGCCCCAGGCGGATATCTCAAGCGCGACTTCCAGGCTGAGAGCGAGGCCCGGGAG	1108
Db	915	CTGAAGGCCCCAGGCGGATATCTCAAGCGCGACTTCCAGGCTGAGAGCGAGGCCCGGGAG	856
Qy	1109	AAGCTGGCGGAGAAAGAGAGTCTCTGCGAGGAGCAGCTGGAGCAGTGCAGAGGGAGTAC	1168
Db	855	AAGCTGGCGGAGAAAGAGAGTCTCTGCGAGGAGCAGCTGGAGCAGTGCAGAGGGAGTAC	796
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Qy	1229	GTGAGAGTCTCCAGGCCCTTTGCCCCCGCCCTGCTACCTCTCTCTCCCTTGGCC	1288
Db	735	GTGAGAGTCTCCAGGCCCTTTGCCCCCGCCCTGCTACCTCTCTCTCCCTTGGCC	676
Qy	1289	CTGCCAGCCAGAGGAGGAGCCCCCGAGGAGCCACTGCATCTCTGCTGCCCAAGTGC	1348
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Qy	1589	GTCCCCCTTTTGGGGTAGATGGCGGCCCGCATCAGGCCTGCATCGCTGCTCTTTTGTTC	1648
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Qy	1649	CCTTCTGCTGCTCGAACCACTTGCTCGGGCTAAATCCCTCCCTCTTCTCCACCCGGCA	1708
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Qy	1709	CTGGGGAAGTCAAGATGGGGCTTGGGGCTCTCAGGGGAGAACTGCTTCCCTCGCAGAGC	1768
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Qy	1889	AGCCAGACCGATGTGATTTTAAACAGTCACTATTGATGGACATTTGGGTGTTTCCCATC	1948
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Db	16	TTTTTTTACCATAA 2	

RESULT 8
AL582339/c
LOCUS

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DEFINITION
AL582339 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL006YE13 3-PRIME, mRNA sequence.

ACCESSION
AL582339

VERSION
AL582339.3 GI:46260808

KEYWORDS
EST.

SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1115)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31320556.
Contact: Genoscope

Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10873.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DL006AC07NP1sc=10873.f.

FEATURES
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                    digested with Not I and cloned into the Not I and EcoR V
                    sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Query Match	47.5%;	Score 948;	DB 1;	Length 1115;
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Matches 973;	Conservative 11;	Mismatches 17;	Indels 2;	Gaps 2;
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QY	1013	GAGCAGCAAGAATTGTGATGAGAGCCGTTCCGGTGCTGAAGGCCCAGGCGGATATCTAC	1072	
DB	951	GAGCAGCAAGAATTGTGATGAGCACSTTCCGGTGCTGAAGSCCCAGSCGATATCTAC	892	
QY	1073	AGGGCGGACTTCAGGCTCAGAGGCGAGCCCGGGAAGCTGGCCGAGAGGAGGAGCTC	1132	
DB	891	AAAGCGCATTCTCAGGCTCAGAGGCGAGSCCGSGAAGCTGCCCGAGAAGAGGAGCTC	832	
QY	1133	CTGCAGGAGCAGCTGGAGCAGCTGCAGAGGGAGTACAGCAAACTGAAGGCCAGCTCTCAG	1192	
DB	831	CTGCAGGAGCAGCTGGAGCAGCTGCAGAGGGAGTACAGCAAACTGAAGGCCAGCTCTCAG	772	
QY	1193	GAGTCGGCCAGGATCGAGACATGAGGAAGCGGCATGTCGAGTCTCCAGGCCCCCTTG	1252	
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ACCESSION AK037020
VERSION AK037020.1 GI:263331883
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
REFERENCE 3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, N., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

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TITLE The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
JOURNAL Functional annotation of a full-length mouse cDNA collection
MEDLINE Nature 409, 685-690 (2001)
PUBMED 11076861
AUTHORS The RIKEN Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 6 (bases 1 to 4535)
PUBMED 11076861
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, N., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216]
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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 DEFINITION Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE005YJ20
 3-PRIME, mRNA sequence.

ACCESSION AL568758

VERSION AL568758.3 GI:46235089

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1081)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 16, 2001 this sequence version replaced gi:30604539.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

into enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 10873.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DE005DE10NP1&c=10873.f.

Location/Qualifiers

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FEATURES
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BX332283
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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COMMENT

On May 2, 2003 this sequence version replaced gi:30339089.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10873.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DC010CC070P1&c=10873.f.

FEATURES

source

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BO674261

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DEFINITION AGENCOURT_8349206 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6276126
5', mRNA sequence.

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ACCESSION

BO674261

VERSION

BO674261.1 GI:21785095

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://img.ncbi.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2460 row: 9 column: 07

High quality sequence stop: 711.

Location/Qualifiers

1..908

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6276126"

/tissue_type="epidermoid carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_102"

/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;

Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed

by Ling Hong in the laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-CDNA

FEATURES

source

synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

```

Query Match 44.0%; Score 877.6; DB 5; Length 908;
Best Local Similarity 99.3%; Pred. No. 1.1e-176;
Matches 902; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
Qy 834 AGTTGCGAGTGGCTTATCACCAGCTCTTCCAAAGATATCGAACACACATCAAGAGCAGCG 893
Db 1 AGTTGCGAGTGGCTTATCACCAGCTCTTCCAAAGATATCGAACACACATCAAGAGCAGCG 60
Qy 894 TGGTGGGAGTGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 953
Db 61 TGGTGGGAGTGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Qy 954 AGGCCGAGGAGGCGCTGGTGGCCAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1013
Db 121 AGGCCGAGGAGGCGCTGGTGGCCAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
Qy 1014 AGCAGCACAGATTGTGATGGAGACCGTTCCGGTGTCTGAAGGCCCGAGCGGATATCTACA 1073
Db 181 AGCAGCACAGATTGTGATGGAGACCGTTCCGGTGTCTGAAGGCCCGAGCGGATATCTACA 240
Qy 1074 AGCCGAGTTCAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1133
Db 241 AGCCGAGTTCAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Qy 1134 TGCGAGGAGCAGCTGAGCAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1193
Db 301 TGCGAGGAGCAGCTGAGCAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy 1194 AGTGGCCAGGATCGAGGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1253
Db 361 AGTGGCCAGGATCGAGGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy 1254 CCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1313
Db 421 CCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Qy 1314 CCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1373
Db 481 CCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Qy 1374 CCCTGCGAGTACATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 1433
Db 541 CCCTGCGAGTACATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 600
Qy 1434 TGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1493
Db 601 TG-CCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 659
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Db 660 AGGATGAAGGGCTGGGTGGCCACAACTGGGATGTCACCTGGAGGCCCGAGGCCCGAGGAGTGG 719
Qy 1554 CCGGGGACCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACG 1613
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Qy 1614 CCCCAGTACAGGCGCTGACTCGCTGCTCTTTTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1673
Db 780 CCCCAGTACAGGCGCTGACTCGCTGCTCTTTTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 838
Qy 1674 CTGGGGTAACTCCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1733
Db 839 CTCGGGTAACTCCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 898
Qy 1734 GGGCTCTC 1741
Db 899 GGGCTCTC 906

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RESULT 14	AL572134/c	913 bp	mRNA	linear	EST 06-APR-2004
LOCUS	AL572134	913 bp	mRNA	linear	EST 06-APR-2004
DEFINITION	AL572134 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1032YJ18 3-PRIME, mRNA sequence.				
ACCESSION	AL572134	GI:12930110			
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 913)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10873.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0D1032YJ18&lc=10873.f.				
FEATURES	Location/Qualifiers				
source	1. 913 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0D1032YJ18" /tissue_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."				
ORIGIN	Query Match 43.5%; Score 866.6; DB 1; Length 913; Best Local Similarity 98.4%; Pred. No. 2.5e-174; Matches 900; Conservative 5; Mismatches 7; Indels 3; Gaps 3;				
QY	1025 ATTGTGATGAGACCGTTCGGTCTGAGAGCCCGAGCGGATATCTACAGGCGGACTTC	1084			
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QY	1085 CAGGCTGAGAGCGAGCGCGGAGAGCTGGCCGAGAGAGAGCTCTCGCAGGAGCAG	1144			
DB	854 CAGGCTGAGAGCGAGCGCGGAGAGCTGGCCGAGAGAGAGCTCTCGCAGGAGCAG	795			
QY	1145 CTGGAGCAGCTGAGAGGAGTACAGAACTGAGGCCAGCTGTGAGGAGTGGCCAGG	1204			
DB	794 CTGGAGCAGCTGAGAGGAGTACAGAACTGAGGCCAGCTGTGAGGAGTGGCCAGG	735			
QY	1205 ATCGAGGACATGAGAGCGGATGCGAGGTCTCCAGGCCCTTGGCCCGCCCTT	1264			
DB	734 ATCGAGGACATGAGAGCGGATGCGAGGTCTCCAGGCCCTTGGCCCGCCCTT	675			
QY	1265 GCCTACTCTCTCTCTCCCTGGCCCTGCGCAGCAGAGGAGGAGCCCGCCGAGGAGCA	1324			
DB	674 GCCTACTCTCTCTCTCCCTGGCCCTGCGCAGCAGAGGAGGAGCCCGCCGAGGAGCA	615			
QY	1325 CCTGACTTCTGCTGCTCCAGTGCAGTATCAGGCCCTTGCATGATGACACCTTGCAGATA	1384			
DB	614 CCTGACTTCTGCTGCTCCAGTGCAGTATCAGGCCCTTGCATGATGACACCTTGCAGATA	555			
QY	1385 CATGTCATGAGTGCATGATGAGGCGCGGCGAGTGCAGGCGCACTGCTGCCCGGAGGAC	1444			
DB	554 CATGTCATGAGTGCATGATGAGGCGCGGCGAGTGCAGGCGCACTGCTGCCCGGAGGAC	496			
QY	1445 GTGCCGGGACCGTGCAGTCTGGCTTCTCTCCGCGCTGCTAGCCAGGATGAGGG	1504			
DB	495 GTGCCGGGACCGTGCAGTCTGGCTTCTCTCCGCGCTGCTAGCCAGGATGAGGG	436			
QY	1505 CTGGGTGGCCACAACTGGGATGCCACTGGAGGCCCAACCCAGGAGCTGGCGCGGACCT	1564			
DB	435 CTGGGTGGCCACAACTGGGATGCCACTGGAGGCCCAACCCAGGAGCTGGCGCGGACCT	376			
QY	1565 TAGCTTCAGCTGTTGATCCGCTGGTCCCTCTTTTGGGGTAGATGCGGCCCGGATCAGG	1624			
DB	375 TAGCTTCAGCTGTTGATCCGCTGGTCCCTCTTTTGGGGTAGATGCGGCCCGGATCAGG	316			
QY	1625 CTTGACTCGCTGCTCTTTTGTTCCTCTGCTGCTCGAACCACTTGGCTCCGGCTTAAT	1684			
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DB	195 GGAGAACTGCTTCCCTCGGAGAGCTGGGTGGGAGCTCTTCTCCACCGGACCGGAC	136			
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QY	1864 TGGGCTGCAATGCTATTTCCATTTTTCAGCCAGACCGATGTGTTATTTAACAGTCACTATTG	1923			
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LOCUS	AL580495	935 bp	mRNA	linear	EST 07-APR-2004
DEFINITION	Homo sapiens cDNA clone CS0D1015YF17 3-PRIME, mRNA sequence.				
ACCESSION	AL580495				
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 935)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On Feb 16, 2001 this sequence version replaced gi:31318767. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10873.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0D1015YF17&lc=10873.f.				
FEATURES	Location/Qualifiers				
source	1. 935 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0D1015YF17"				

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 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN

Query Match 43.1%; Score 859.2; DB 1; Length 935;
 Best Local Similarity 95.1%; Pred. No. 9.4e-173;
 Matches 884; Conservative 22; Mismatches 22; Indels 2; Gaps 2;

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Qy	1143	AGCTGGAGAGCTGCGAGAGGAGTA CAGCAAACTGAAGCCAGCTGT CAGGAGTCGGCCA	1202
Db	816	AGCTGGAGAGCTGCGAGAGGAGTA CAGCAAACTGAAGCCAGCTGT CAGGAGTCGGCCA	757
Qy	1203	GGATCGAGGACATGAGAGCGGATGCGAGTCTCCAGGCGCCCTTGGCCCCCGGCC	1262
Db	756	GGATCGAGGACATGAGAGCGGATGCGAGTCTCCAGGCGCCCTTGGCCCCCGGCC	697
Qy	1263	CTGCTACCTCTCTCTCTCCCTTGGCCCTGCCCAGCCAGAGGAGCGCCCGCCGAGGAGC	1322
Db	696	CTGCTACCTCTCTCTCTTTTGGCCCTGCCCAGCCAGAGGAGCGCCCGCCGAGGAGC	637
Qy	1323	CACCTGACTTCTGCTGCCAAGTCCAGTATCAGGCCCCCTGATATGGAACCCCTGCAGA	1382
Db	636	CACCTGACTTCTGCTGCCAAGTCCAGTATCAGGCCCCCTGATATGGAACCCCTGCAGA	577
Qy	1383	TACATGTATGAGTGCATTGAGTAGGGCCGCGCAGTGCAGGCCACCTGCTGCCCGAGG	1442
Db	576	TACATGTATGAGTGCATTGAGTAGGGCCGCGCAGTGCAGGCCACCTGCTGCCCGAGG	518
Qy	1443	ACGTGCCCGGACCGTGCAGTCTGGCTTTCTCTCCGCTGCTAGCCCGCAGGATGAAG	1502
Db	517	ACGTGCCCGGACCGTGCAGTCTGGCTTTCTCTCCGCTGCTAGCCCGCAGGATGAAG	458
Qy	1503	GGCTGGGTGGCCACACTGGATGCCACCTGGAGCCGACCCAGGAGCTGGCCGGGCAC	1562
Db	457	GGCTGGGTGGCCACACTGGATGCCACCTGGAGCCGACCCAGGAGCTGGCCGGGCAC	398
Qy	1563	CTTACGCTTCAGTGTGATCCGCTGGTCCCTCTTTTGGGTAGATCGGCCCGCGATCA	1622
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Qy	1623	GGCTGACTCGTCTCTTTTGTTCCTCTCTGCTGCTCGAACCATTTGCTCGGGCTA	1682
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Qy	1683	ATCCCTCCCTCTCTCTCCACCGGACCTGGGAACTCAAGAAATGGGGCTGGGGCTCTCA	1742
Db	277	ATCCCTCCCTCTCTCTCCACCGGACCTGGGAACTCAAGAAATGGGGCTGGGGCTCTCA	218
Qy	1743	GGGAGAACTGCTTCCCTGGGAGAGCTGGGTGGAGCTCTTCTCCACCGGACACCGAC	1802
Db	217	GGGAGAACTGCTTCTCTGGGAGAGCTGGGTGGAGCTCTTCTCCACCGGACACCGAC	158
Qy	1803	CGGCCCGGCTGTGCTCTGGGAGTGTGCTCTTACCATGACACGGGTGCTCTCTT	1862
Db	157	CGGCCCGGCTGTGCTCTGGGAGTGTGCTCTTACCATGACACGGGTGCTCTCTT	98
Qy	1863	TTGGGCTGCACTATTCCATTTTCAGCCAGACCGATGTGTATTTAACAGTCACTATT	1922
Db	97	TTGGGCTGCACTATTCCATTTTCAGCCAGACCGATGTGTATTTAACAGTCACTATT	38

Qy 1923 GATGACATTTGGGTTGTTTCCCATCTTTT 1952
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 Db 37 GATGACATTTGGGTTGTTTCCCATCTTTT 8
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Search completed: February 9, 2005, 02:52:26
 Job time : 6682 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 12:25:23 ; Search time 1097 Seconds

(without alignments)
10760.223 Million cell updates/sec

Title: US-09-377-795-1

Perfect score: 1994

Sequence: 1 ggcacgagcatggcccttgt.....gtataaaaaaaaaaaaaa 1994

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1994	100.0	1994	3	AAC81426 Human I-k
2	1994	100.0	1994	3	AAA35027 Human ade
3	1994	100.0	1994	3	Aaf21149 Human low
4	1994	100.0	1994	8	ADA44705 Human inh
5	1994	100.0	1994	10	ABZ96843 Human nuc
6	1994	100.0	1994	10	ABV75393 Human NEM
7	1994	100.0	1994	11	ABD20692 Human pul
8	1994	100.0	8631	3	AAA35028 Human ade
9	1994	100.0	8631	3	Aaf21150 Human low
10	1994	100.0	8631	10	ABZ96844 Human nuc
11	1992.4	99.9	8631	11	ABD20693 Human pul
12	1954.4	98.0	1967	13	ADQ87415 Human tum
13	1954.4	98.0	1967	13	ADQ86256 Human tum
14	1836.4	92.1	2035	8	ACD23012 Human NEM
15	1832.6	91.9	1975	8	ADA44712 Human inh
16	1823	91.4	2009	2	AAZ07513 Human RIP
17	1757.2	88.1	2034	2	AAZ07514 Human RIP
18	1358.6	68.1	2038	10	ADP82713 Leukaemia
19	1253.6	62.9	1260	12	ADK71964 Human I K
20	941	47.2	1104	13	ADS17862 Human IKB

21	940.4	47.2	1874	10	ADC36537	Adc36537 DNA encod	
22	940.4	47.2	1874	12	ADI61940	Adi61940 Necrosis	
23	940.4	47.2	1874	12	ADI29002	Adi29002 Human NEM	
24	940.4	47.2	1874	13	ADI61943	Adi61943 Necrosis	
25	705.8	35.4	23106	9	ACD23011	ACD23011 Human NEM	
26	486	24.4	486	13	ADS17866	Adsi17866 Human IKB	
27	402.6	20.2	483	13	ADS17864	Adsi17864 Human IKB	
c	28	277.6	13.9	2803	3	Aaf21697	Aaf21697 Human bre
29	262	13.1	337	10	ADF81343	Adf81343 Leukaemia	
30	216	10.8	597	12	ACH79507	Ach79507 Human gen	
31	212	10.6	236	9	ACH15127	Ach15127 Human adu	
32	207.4	10.4	526	12	ACH76707	Ach76707 Human gen	
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34	195.4	9.8	197	12	ACH90407	Ach90407 Human gen	
35	187	9.4	264	13	ADS17868	Adsi17868 Human IKB	
c	36	155.6	7.8	30191	12	ADQ97654	Adq97654 Mouse can
37	137	6.9	1926	3	AAAS0254	Aaas0254 Epstein B	
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40	137	6.9	2580	3	AAA75454	Aaa75454 Nucleotid	
41	137	6.9	2580	6	AAI64275	Aai64275 Epstein-B	
c	42	137	6.9	5452	2	AAx90923	Aax90923 Anti-sens
c	43	137	6.9	8705	2	AAZ23778	Aaz23778 Vector ps
c	44	137	6.9	8705	12	ADM10659	Adm10659 Expressio
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ALIGNMENTS

RESULT 1

AAC81426

ID AAC81426 standard; cDNA; 1994 BP.

XX AAC81426;

XX 23-FEB-2001 (first entry)

XX Human I-kappa-B kinase gamma-subunit (IKK-gamma) cDNA.

XX Human; I-kappa-B kinase; IKK; antisense therapy; gene therapy;

KW cytokine expression inhibition; NF-kappa-B activation inhibition;

KW nuclear factor-kappa-B; rheumatoid arthritis; immune disorder; cancer;

KW IKK-gamma; gamma-subunit; ss.

XX Homo sapiens.

OS JP2000253884-A.

XX 19-SEP-2000.

XX 10-MAR-1999; 99JP-00063291.

XX 10-MAR-1999; 99JP-00063291.

XX (TOAG) TOA COSEI CHEM IND LTD.

XX WPI; 2000-658913/64.

XX Antisense nucleic acid compound complementary to the subunit of IkappaB,

XX used to treat rheumatic arthritis, immune diseases and cancer.

XX Claim 3; Page 14-15; 20pp; Japanese.

XX The invention relates to an antisense oligonucleotide targetted to a gene

CC encoding a subunit of I-kappa-B kinase (IKK) which inhibits its

CC expression, and thereby inhibits expression of a cytokine such as IL-6

CC (interleukin-6). I-kappa-B kinase activates NF-kappa-B (nuclear factor-

CC kappa-B) which acts a transcriptional regulator of cytokine genes. The

CC antisense oligonucleotide can be used in gene therapy to treat rheumatoid

CC arthritis, immune disorders and cancers. Sequences AAC81422-C81426 are

CC cDNAs derived from genes whose expression may be inhibited using an

CC antisense oligonucleotide of the invention. The present sequence

CC	represents a human IKK-gamma subunit cDNA														
XX	Sequence	1994	BP:	429	A;	585	C;	633	G;	347	T;	0	U;	0	Other;
SQ	Query Match	100.0%; Score 1994; DB 3; Length 1994;													
	Best Local Similarity	100.0%; Pred. No. 0;													
	Matches 1994; Conservative	0; Mismatches 0; Indels 0; Gaps 0;													
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DB	1	GGCAGCAGCATGCCCTTTGTGATCCAGGTGGGAAACTTAAGGCCCCAGAGAAAGTAGGAGCC	60												
QY	61	CCGACAGACTATCAATCCCACTCTTCCCTCACTCCCTGTGAAGCTCTCCAGCATATC	120												
DB	61	CCGACAGACTATCAATCCCACTCTTCCCTCACTCCCTGTGAAGCTCTCCAGCATATC	120												
QY	121	GAGGTCCCATACGCCCCCTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTG	180												
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QY	361	TCCTGGGAGCGCTCGGAGGAGCTTCTGCAATTCACAGCCAGCCAGGAGGAGAGGA	420												
DB	361	TCCTGGGAGCGCTCGGAGGAGCTTCTGCAATTCACAGCCAGCCAGGAGGAGAGGA	420												
QY	421	GTTCTCTATGTGCAAGTTTCCAGGAGCCAGGAAACTGGTGAGAGACTCGGCCCTGGAGAA	480												
DB	421	GTTCTCTATGTGCAAGTTTCCAGGAGCCAGGAAACTGGTGAGAGACTCGGCCCTGGAGAA	480												
QY	481	GCTCGATCTGAAGAGGCGAGAGGAGAGGCTCTCGGAGAGTGGAGCACTTGAAGAGATG	540												
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DB	661	GGGTGGGCGCGCGCCAGGAGCAGGCGCGGAGCTGAGAGTGAAGCGCGAGGCGCT	720												
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DB	721	GCAGCAGCAGCAGCAGCTGCAAGTGGAGTGCAGCTGGCATGCAAGGCGCAGAGCGTGGAGGC	780												
QY	781	CGCGTCCGCATGGAGCCAGGCGCGCTCGGAGGAGAGAGGAGCTGGCCCACTTGA	840												
DB	781	CGCGTCCGCATGGAGCCAGGCGCGCTCGGAGGAGAGAGGAGCTGGCCCACTTGA	840												
QY	841	GGTGGCCTATCAGCAGCTCTTCCAGATACGCAACCAATCAAGAGCAGCGTGGTGGG	900												
DB	841	GGTGGCCTATCAGCAGCTCTTCCAGATACGCAACCAATCAAGAGCAGCGTGGTGGG	900												
QY	901	CAGTGAGCGGAGGAGGAGATGCAAGTGGAGATCTTCAAAACAGCAGCTCCAGCAGGCCGA	960												
DB	901	CAGTGAGCGGAGGAGGAGATGCAAGTGGAGATCTTCAAAACAGCAGCTCCAGCAGGCCGA	960												
QY	961	GGAGGCCCTGTGGCCAAACAGGAGGTGATCGATAAGCTGAAGAGGAGGCCGAGCAGCA	1020												

RESULT 2

AAA35027	Human adenosine receptor related polynucleotide SEQ ID NO:2716.
ID	AAA35027 standard; DNA; 1994 BP.
XX	AAA35027;
AC	28-JUL-2000 (first entry)
XX	Human adenosine receptor related polynucleotide SEQ ID NO:2716.
DT	Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX	phosphorothioate; impaired respiration; inflammation; allergy;
XX	allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX	antiallergic; antasthmatic; cyostatic; analgesic; impaired airway;
XX	lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX	respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX	pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX	cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
OS	Homo sapiens.
XX	WO200009525-A2.
PN	24-FEB-2000.
XX	03-AUG-1999; 99WO-US017712.
PF	03-AUG-1998; -98US-0095212P.
XX	(UYEC-) UNIV EAST CAROLINA.
PA	Nyce JW;
XX	WPI; 2000-205971/18.
PI	New antisense oligonucleotides useful for treating e.g. pulmonary
DR	vasoconstriction, inflammation, allergies, asthma, hypertension,
XX	bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX	cancers.
PT	Disclosure; Page 968-969; 1343pp; English.
PT	The present invention describes a new composition comprising an antisense
CC	oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC	nucleic acids involved in bronchoconstriction, allergies, and/or
CC	inflammation. The ON can have antiinflammatory, antiallergic,
CC	antasthmatic, cyostatic and analgesic activities. The compositions are
CC	useful for the treatment of diseases associated with inflammation,
CC	impaired airways, including lung disease and diseases whose secondary
CC	effects afflict the lungs of a subject. They can be used for treating
CC	e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC	impaired respiration, respiratory distress syndrome, pain, cystic
CC	fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC	pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC	carcinomas, and cancers which may metastasize to the lungs, including
CC	breast and prostate cancer. The reduction of the adenosine content of the
CC	ONs reduces side effects. The A-containing ONs break down with the
CC	release of deoxyadenosine which activates adenosine receptors causing
CC	bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC	nucleotide sequences given in the sequence listing from the present
CC	invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC	sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC	from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC	AAA33992) are specifically claimed ONs from the present invention. N.B.
CC	Sequences given in the disclosure of the present invention do not match
CC	up with their corresponding SEQ ID NO: sequences given in the sequence
CC	listing
XX	Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;
XX	Query Match 100.0%; Score 1994; DB 3; Length 1994;
XX	Best Local Similarity 100.0%; Pred. No. 0;
XX	Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

DEC 17 1963

RESULT 3
DATE 11/19

AAF21149
ID AAF21149 standard; DNA: 1994 BP.

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AC AAF21149:

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DT 14-MAR-2001 (first entry)

XX

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory bronchodilator; antiinflammatory; immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; ROS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

Homo sapiens.

WO200062736-A2

26-OCT-2000

24-MAR-2000; 2000WO-US008020.

06-APR-1999; 99US-0127958P.

(UYEC-) UNIV EAST CAROLINA

(NYCE//) NYCE J W.

Nyce JW:

WPI: 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Disclosure: Page 1045-1046: 1592pp: English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS) pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 1994 BP: 429 A: 585 C: 633 G: 347 T: 0 U: 0 Other:

every Match	100.0%	Score 1994:	DB 3:	Length 1994:
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	Pred. No. 0;
100.0%;	100.0%;
most Local Similarity	100.0%;

Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 GGCACGAGCATGGCCCTTGTGATCCAGGTGGGAACTAAGGCCCAGAGAAGTGAGGACC 60

Db 1 GGACAGCATGGCCCTTGTGATCCAGGTGGGAAACTAAGGCCCCAGAGAACTGAGGACC 60
Qy 61 CCGCAGACTATCAATCCAGTCTCTTCCCTCACTCCCTGTGAAGCTCTCCAGCATATC 120
Db 61 CCGCAGACTATCAATCCAGTCTCTTCCCTCACTCCCTGTGAAGCTCTCCAGCATATC 120
Qy 121 GAGGTCCCATCAGCCCTTCCCTGTGATGAATAGGCACCTCTGGAGAGCAACTGTG 180
Db 121 GAGGTCCCATCAGCCCTTCCCTGTGATGAATAGGCACCTCTGGAGAGCAACTGTG 180
Qy 181 TGAGATGTGACGCCAGTGTGGCCCGGCAGCAGATCAGAGCTGTGAGGCGAAGATGC 240
Db 181 TGAGATGTGACGCCAGTGTGGCCCGGCAGCAGATCAGAGCTGTGAGGCGAAGATGC 240
Qy 241 TCCCTCTGGGGAAGCAGACCATGCTGCACCTGCTTTCAGAAACAGGGCGCTCTGAGACCT 300
Db 241 TCCCTCTGGGGAAGCAGACCATGCTGCACCTGCTTTCAGAAACAGGGCGCTCTGAGACCT 300
Qy 301 CCAGCGCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACAGAT 360
Db 301 CCAGCGCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACAGAT 360
Qy 361 TCTGCGGAGCGCTGCGAGGAGCTTCTGATTTTCAAGCCAGCAGAGGAGGAGAA 420
Db 361 TCTGCGGAGCGCTGCGAGGAGCTTCTGATTTTCAAGCCAGCAGAGGAGGAGAA 420
Qy 421 GTTCTCATGTGCAAGTTCCAGGAGCCAGGAACTGGTGGAGAGACTCGGCTTGAGAA 480
Db 421 GTTCTCATGTGCAAGTTCCAGGAGCCAGGAACTGGTGGAGAGACTCGGCTTGAGAA 480
Qy 481 GCTCGATCTGAAGAGCAGAGGAGCAGGCTCTCGGGAGGTGGAGACCTCAAGAGATG 540
Db 481 GCTCGATCTGAAGAGCAGAGGAGCAGGCTCTCGGGAGGTGGAGACCTCAAGAGATG 540
Qy 541 CCAGCAGCAGATGGCTGAGGAAAGGCTCTGTGAAAGCCAGAGTGAAGTCTTGTGCG 600
Db 541 CCAGCAGCAGATGGCTGAGGAAAGGCTCTGTGAAAGCCAGAGTGAAGTCTTGTGCG 600
Qy 601 GGAGCTGCAAGGAGAGCAGAGTGGCTGGAGGCTGCCATAGGAATGCCAGGCTCTGGA 660
Db 601 GGAGCTGCAAGGAGAGCAGAGTGGCTGGAGGCTGCCATAGGAATGCCAGGCTCTGGA 660
Qy 661 GGGTGGGCGCCGGGGGCGCAGCAGCAGCGCGGAGCTGGAGAGTGAAGCGAGCGCT 720
Db 661 GGGTGGGCGCCGGGGGCGCAGCAGCAGCGCGGAGCTGGAGAGTGAAGCGAGCGCT 720
Qy 721 GCAGCAGCAGCAGCGGTGAGGATGACAGCTGCGCATGCGAGGCGCAGAGCGTGGAGGC 780
Db 721 GCAGCAGCAGCAGCGGTGAGGATGACAGCTGCGCATGCGAGGCGCAGAGCGTGGAGGC 780
Qy 781 CCGGCTCCGATGGAGCGCCAGCGCGCTCGGAGGAGAGAGAGCTGGCCAGTTGCA 840
Db 781 CCGGCTCCGATGGAGCGCCAGCGCGCTCGGAGGAGAGAGAGCTGGCCAGTTGCA 840
Qy 841 GGTGGCTATCACCAGCTCTTCCAGAAATACACAAACCAATCAAGAGCAGCGTGGTGG 900
Db 841 GGTGGCTATCACCAGCTCTTCCAGAAATACACAAACCAATCAAGAGCAGCGTGGTGG 900
Qy 901 CAGTGAGCGGAAGCGAGGAATCAGCTGGAAGATCTCAAAACAGCAGCTCCAGAGCGCGA 960
Db 901 CAGTGAGCGGAAGCGAGGAATCAGCTGGAAGATCTCAAAACAGCAGCTCCAGAGCGCGA 960
Qy 961 GGAGGCTTGGTGGCCCAACAGAGGTGATCATAGCTGAAGGAGGAGGCGCGAGCAGCA 1020
Db 961 GGAGGCTTGGTGGCCCAACAGAGGTGATCATAGCTGAAGGAGGAGGCGCGAGCAGCA 1020
Qy 1021 CAAGATTGTGATGGAGACCGCTTCCGCTGTGAAGGCCAGCGGATATCTACAAGCGGA 1080
Db 1021 CAAGATTGTGATGGAGACCGCTTCCGCTGTGAAGGCCAGCGGATATCTACAAGCGGA 1080
Qy 1081 CTTCCAGGCTGAGAGCAGCGCCCGGAGAAAGCTGGCCGAGAAAGAGGAGCTCTTCAGGA 1140
Db 1081 CTTCCAGGCTGAGAGCAGCGCCCGGAGAAAGCTGGCCGAGAAAGAGGAGCTCTTCAGGA 1140

RESULT 4
ADA44705

ID ADA44705 standard; DNA; 1994 BP.

XX ADA44705;

XX 20-NOV-2003 (first entry)

DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 3.

XX Antisense oligonucleotide; cytostatic; immunosuppressive;

KW antiinflammatory; gene therapy; hyperproliferative disorder; cancer;
 KW autoimmune; inflammatory disorder; inhibitor-kappa B kinase-gamma; gene;
 XX ds.

OS Homo sapiens.

PN WO2003031576-A2.

PD 17-APR-2003.

PF 03-OCT-2002; 2002WO-US031809.

PR 06-OCT-2001; 2001US-00972607.

PA (ISIS-) ISIS PHARM INC.

XX Monia BP, Wyatt JP;

XX WPI; 2003-457242/43.

DR New compound having sequence targeted to nucleic acid encoding inhibitor-
 PT kappa B kinase-gamma, useful for preparing composition for treating e.g.,
 PT cancer, or inflammatory or autoimmune disorder.

PS Example 15; Page 82-85; 106pp; English.

XX The invention relates to an antisense compound that is targeted to a
 CC nucleic acid encoding inhibitor-kappa B kinase-gamma, specifically
 CC hybridizing to the nucleic acid encoding inhibitor-kappa B kinase-gamma
 CC and inhibiting its expression. Compounds of the invention are antisense
 CC oligonucleotides comprising at least one modified internucleoside
 CC linkage, which is a phosphorothioate linkage, at least one modified sugar
 CC moiety, which is a 2'-O-methoxyethyl sugar moiety, or at least one
 CC modified nucleobase, which is a 5-methylcytosine. Preferably, the
 CC antisense oligonucleotide is a chimeric oligonucleotide. The compound of
 CC the invention is useful for preparing a composition for treating a
 CC hyperproliferative disorder e.g., cancer, or an autoimmune or
 CC inflammatory disorder. The methods are useful for inhibiting the
 CC expression of inhibitor-kappa B kinase-gamma in cells or tissues, and
 CC treating an animal having a disease or condition associated with
 CC inhibitor-kappa B kinase-gamma. The current sequence represents the human
 CC inhibitor-kappa B kinase-gamma encoding sequence that was used to design
 CC the antisense oligonucleotides of the invention.

XX Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

Query Match 100.0%; Score 1994; DB 8; Length 1994;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGCAGAGATGGCCCTTGTGATCCAGGTGGGAAACTAAGGCCCAGAGAAGTGAGGACC	60
Db	1	GGCAGAGATGGCCCTTGTGATCCAGGTGGGAAACTAAGGCCCAGAGAAGTGAGGACC	60
QY	61	CCGACAGATCAATCCAGTCTCTCCCTCACTCCCTGTGAAGTCTCCAGCATATC	120
Db	61	CCGACAGATCAATCCAGTCTCTCCCTCACTCCCTGTGAAGTCTCTCCAGCATATC	120
QY	121	GAGGTCCCATCAGCCCTTGGTGTGAATAGGACCTCTGGAAGAGCCAACTGTG	180
Db	121	GAGGTCCCATCAGCCCTTGGTGTGAATAGGACCTCTGGAAGAGCCAACTGTG	180
QY	181	TCAGATGTGACGCCAGTGTGGCCCGGAGCAGATCAGAGATGAGGAGGAGGAGG	240
Db	181	TCAGATGTGACGCCAGTGTGGCCCGGAGCAGATCAGAGATGAGGAGGAGGAGG	240
QY	241	TCCTCTGGGGAAGCAGCCATGTGTCACCTGCTTCAACAGCGGCTCTTGAACCT	300
Db	241	TCCTCTGGGGAAGCAGCCATGTGTCACCTGCTTCAACAGCGGCTCTTGAACCT	300
QY	301	CCAGCGTGTCTGAGGAGATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACAGAT	360
Db	301	CCAGCGTGTCTGAGGAGATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACAGAT	360

QY	361	TCTCGGAGAGCGCTCCGAGAGCTTCTGCAATTTCCAGCCAGCCAGAGGAGGAGGA	420
Db	361	TCTCGGAGAGCGCTCCGAGAGCTTCTGCAATTTCCAGCCAGCCAGAGGAGGAGGA	420
QY	421	GTTCTCATGTGCAAGTTCCAGGAGGCCAGGAAACTGGTGAGAGACTCGGCTCGAGAA	480
Db	421	GTTCTCATGTGCAAGTTCCAGGAGGCCAGGAAACTGGTGAGAGACTCGGCTCGAGAA	480
QY	481	GCTCGATCTGAAGAGCAGAGAGGAGGAGGCTCTCGGGAGGTGAGACACCTGAAGATG	540
Db	481	GCTCGATCTGAAGAGCAGAGAGGAGGAGGCTCTCGGGAGGTGAGACACCTGAAGATG	540
QY	541	CCAGCAGCAGATGGCTGAGGACCAAGGCTCTGTGAAAGCCAGGTGAGCTCTTCTCGG	600
Db	541	CCAGCAGCAGATGGCTGAGGACCAAGGCTCTGTGAAAGCCAGGTGAGCTCTTCTCGG	600
QY	601	GGAGCTGCAGGAGAGCCAGAGTCTGAGGCTGCTGAGGCTGCTGAGGCTCTGGA	660
Db	601	GGAGCTGCAGGAGAGCCAGAGTCTGAGGCTGCTGAGGCTGCTGAGGCTCTGGA	660
QY	661	GGGTTCGGGCCCCGGGCGGCGCAGCAGCAGGCGCGGCGCTGAGAGTCTGAGCGCGGCT	720
Db	661	GGGTTCGGGCCCCGGGCGGCGCAGCAGCAGGCGCGGCGCTGAGAGTCTGAGCGCGGCT	720
QY	721	GCAGCAGCAGCAGCAGCGTGCAGGTGGACACAGCTGCGCATCCAGGCCAGAGCGTGGAG	780
Db	721	GCAGCAGCAGCAGCAGCGTGCAGGTGGACACAGCTGCGCATCCAGGCCAGAGCGTGGAG	780
QY	781	CGCGCTCCGATCGAGCGCGGCGCAGCAGCAGGCGCGGCGCTGAGAGTCTGAGCGCGGCT	840
Db	781	CGCGCTCCGATCGAGCGCGGCGCAGCAGCAGGCGCGGCGCTGAGAGTCTGAGCGCGGCT	840
QY	841	GTTGGCTTATCACCACTCTTCCAGAATACGACCAACCATCAAGAGCAGCGTGGTGGG	900
Db	841	GTTGGCTTATCACCACTCTTCCAGAATACGACCAACCATCAAGAGCAGCGTGGTGGG	900
QY	901	CAGTGAAGCGGAGGAGGAGTCTGAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	960
Db	901	CAGTGAAGCGGAGGAGGAGTCTGAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG	960
QY	961	GGAGGCGCTGTGGTGGCCAAACAGGAGGTGATCGAATAAGCTGAAGAGGAGGCGGAGCAG	1020
Db	961	GGAGGCGCTGTGGTGGCCAAACAGGAGGTGATCGAATAAGCTGAAGAGGAGGCGGAGCAG	1020
QY	1021	CAAGATTGTGATGAGACCGTTCGGTGTCTGAAGGCCAGGCGGATATCTACAAGGCGGA	1080
Db	1021	CAAGATTGTGATGAGACCGTTCGGTGTCTGAAGGCCAGGCGGATATCTACAAGGCGGA	1080
QY	1081	CTTCCAGGCTGAGAGGAGGCGGCGGAGAGGCTGGCCGAGAGAGGAGGCTCTCTGAGGA	1140
Db	1081	CTTCCAGGCTGAGAGGAGGCGGCGGAGAGGCTGGCCGAGAGAGGAGGCTCTCTGAGGA	1140
QY	1141	GCAGTGGAGCAGCTGTCAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGGAGTCTGGC	1200
Db	1141	GCAGTGGAGCAGCTGTCAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGGAGTCTGGC	1200
QY	1201	CAGGATCCAGGAGCATGAGGAGGCGGCTGAGGCTCTCCAGGCGGCTCTGCGGCGGCGG	1260
Db	1201	CAGGATCCAGGAGCATGAGGAGGCGGCTGAGGCTCTCCAGGCGGCTCTGCGGCGGCGG	1260
QY	1261	CCCTGCCTACCTCTCTCTCTCCCTGGCCCTGCGCAGCAGAGGAGGAGGCGGCGGCGG	1320
Db	1261	CCCTGCCTACCTCTCTCTCTCCCTGGCCCTGCGCAGCAGAGGAGGAGGCGGCGGCGG	1320
QY	1321	GCCACTGACTTCTGCTGTCCCAAGTGCAGATCAGGCGGCTGTATGAGACACCTGCA	1380
Db	1321	GCCACTGACTTCTGCTGTCCCAAGTGCAGATCAGGCGGCTGTATGAGACACCTGCA	1380
QY	1381	GATACATGTGATGAGTGCATTGAGTGGCGGCGGCTGAGTGGCGGCGGCTGAGTGGCGG	1440
Db	1381	GATACATGTGATGAGTGCATTGAGTGGCGGCGGCTGAGTGGCGGCGGCTGAGTGGCGG	1440

Db 1981 AAAAAAAAAAAAAA 1994

RESULT 7

ABD20692

ID ABD20692 standard; DNA; 1994 BP.

AC ABD20692;

XX 29-JUL-2004 (first entry)

XX Human pulmonary and inflammatory target DNA #303.

DE Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;

XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;

KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;

KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;

KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;

KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;

KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;

XX pulmonary transplantation rejection; ds.

OS Homo sapiens.

XX W020285309-A2.

EN 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIC-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasegna A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shanabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense

PT oligonucleotide containing less percentage of adenosine, targeted to

PT nucleic acids associated with lung airway or lung dysfunction, and

PT bronchodilating agent.

XX Claim 15; SEQ ID NO 12085; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,

CC comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and

CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,

CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating

CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC The invention also describes a kit, that comprises: (a) a delivery

CC device, in separate containers, (b) the oligonucleotides, (c)

CC instructions for adding a carrier and for use of the kit. The composition

CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,

CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a

CC beta-adrenergic agonist. The composition is useful for preventing or

CC treating a respiratory, lung or malignant disease. The administered

CC composition comprises oligo and is administered to reduce the production

CC or availability, or to increase the degradation of the target mRNA or to

CC reduce the amount of target polypeptide present in the lungs. The

CC pulmonary obstruction, and/or bronchoconstriction and/or lung

CC inflammation, allergies and/or surfactant hypoproduction are associated

CC with a disease or condition such as pulmonary vasoconstriction,

CC inflammation, allergies, asthma, impeded respiration, respiratory

CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary

CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary

CC transplantation rejection, pulmonary infections, bronchitis or cancer.

CC The reduced adenosine content of the anti-sense oligos corresponding to

CC thymidines present in the target RNA serves to prevent the breakdown of

CC the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to

CC prevent any unwanted effects due to it

XX

XX Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

Query Match 100.0%; Score 1994; DB 11; Length 1994;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACGAGCATGGCCCTTGTCATCCAGTGGGGAACTAAGCCCCAGAGAAGTAGGACC 60

DB 1 GGCACGAGCATGGCCCTTGTCATCCAGTGGGGAACTAAGCCCCAGAGAAGTAGGACC 60

QY 61 CCGCAGACTATCAATCCAGTCTCTTCCCTCTCACTCCCTGTGAAGCTCTCCAGCATCATC 120

DB 61 CCGCAGACTATCAATCCAGTCTCTTCCCTCTCACTCCCTGTGAAGCTCTCCAGCATCATC 120

QY 121 GAGTCCCATCAGCCCTTGGCTTTGGATGAATAGGACCTCTGGAAGAGCAACTGTG 180

DB 121 GAGTCCCATCAGCCCTTGGCTTTGGATGAATAGGACCTCTGGAAGAGCAACTGTG 180

QY 181 TGAGATGGTGCAGCCAGTGGTGGCCGCGCAGCAGATCAGGACCTACTGGGCGAGATC 240

DB 181 TGAGATGGTGCAGCCAGTGGTGGCCGCGCAGCAGATCAGGACCTACTGGGCGAGATC 240

QY 241 TCCTCTGGGGAAGCCAGCCATGCTGCACCTTGCCTTCAGAACAGGGCGCTCTCTGAGCCCT 300

DB 241 TCCTCTGGGGAAGCCAGCCATGCTGCACCTTGCCTTCAGAACAGGGCGCTCTCTGAGCCCT 300

QY 301 CCAGCGCTGCTCGAGGAGGAATCAAGAGCTCCGAGATGCCATCCGCGCAGCAGCAACCAT 360

DB 301 CCAGCGCTGCTCGAGGAGGAATCAAGAGCTCCGAGATGCCATCCGCGCAGCAGCAACCAT 360

QY 361 TCTGCGGGAGCGCTGCGAGGAGCTTCTGCAATTTCCAAAGCCAGAGGAGGAGGAAGGA 420

DB 361 TCTGCGGGAGCGCTGCGAGGAGCTTCTGCAATTTCCAAAGCCAGAGGAGGAGGAAGGA 420

QY 421 GTTCTCTATGTCAAGTTCCAGAGGCGCAGGAACTGGTGGAGAGACTCGGCTCTGGAGAA 480

DB 421 GTTCTCTATGTCAAGTTCCAGAGGCGCAGGAACTGGTGGAGAGACTCGGCTCTGGAGAA 480

QY 481 GCTCGATCTGAAGAGGCGCAGAGGAGCTCTGCGGAGGTGGAGCACCTGAGAGATG 540

DB 481 GCTCGATCTGAAGAGGCGCAGAGGAGCTCTGCGGAGGTGGAGCACCTGAGAGATG 540

QY 541 CCAGCAGCAGATGGCTGAGGAGCAAGGCTCTGTGAAAGCCAGGTGACGCTCTTGCTCGG 600

DB 541 CCAGCAGCAGATGGCTGAGGAGCAAGGCTCTGTGAAAGCCAGGTGACGCTCTTGCTCGG 600

QY 601 GGAGCTGCGAGGAGGCGCAGAGTGGCTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGA 660

DB 601 GGAGCTGCGAGGAGGCGCAGAGTGGCTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGA 660

QY 661 GGGTCCGGGCGCCGCGGCGCAGGAGCAGCGCGGCGAGCTGGAGAGTCCAGCGCGCT 720

DB 661 GGGTCCGGGCGCCGCGGCGCAGGAGCAGCGCGGCGAGCTGGAGAGTCCAGCGCGCT 720

QY 721 GCAGCAGCAGCAGCGCTGCGAGTGGAGCCAGCTGCGCATGCGAGGCGCAGAGCGTGGAGGC 780

DB 721 GCAGCAGCAGCAGCGCTGCGAGTGGAGCCAGCTGCGCATGCGAGGCGCAGAGCGTGGAGGC 780

QY 781 CCGGCTCCGCATGAGGCGCGCAGCGCTCGGAGGAGGAGGAAGCTGCGCCAGTGGCA 840

DB 781 CCGGCTCCGCATGAGGCGCGCAGCGCTCGGAGGAGGAGGAAGCTGCGCCAGTGGCA 840

QY 841 GTTGGCTATACAGCTCTTCCAAAGAATACGACACCATCAAGAGCAGCGTGGTGGG 900

DB 841 GTTGGCTATACAGCTCTTCCAAAGAATACGACACCATCAAGAGCAGCGTGGTGGG 900

QY 901 CAGTGGCGGAGCGGAGGAGTCCAGCTGGAAGATCTCAAAACAGCAGCTCCAGAGGCCGA 960

DB 901 CAGTGGCGGAGCGGAGGAGTCCAGCTGGAAGATCTCAAAACAGCAGCTCCAGAGGCCGA 960

QY 961 GGAGGCCCTGTGGCCCAACAGGAGGTGATCGATAAGCTGAAGGAGGAGGCCGAGCAGCA 1020
 DB |||||
 QY 961 GGAGGCCCTGTGGCCCAACAGGAGGTGATCGATAAGCTGAAGGAGGAGGCCGAGCAGCA 1020
 DB |||||
 QY 1021 CAAGATTGTGTGAGAGACCGCTTCCGGTGTGAAGGCCAGCGGATATCTCAAGGCCGA 1080
 DB |||||
 QY 1021 CAAGATTGTGTGAGAGACCGCTTCCGGTGTGAAGGCCAGCGGATATCTCAAGGCCGA 1080
 DB |||||
 QY 1081 CTTCCAGGCTGAGAGCGAGCCCGGAGAGCTGCGAGAGAGAGGAGCTCCTCGAGCA 1140
 DB |||||
 QY 1081 CTTCCAGGCTGAGAGCGAGCCCGGAGAGCTGCGAGAGAGAGGAGCTCCTCGAGCA 1140
 DB |||||
 QY 1141 GCAGCTGGAGCAGCTGCGAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGAGTTCGCG 1200
 DB |||||
 QY 1141 GCAGCTGGAGCAGCTGCGAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGAGTTCGCG 1200
 DB |||||
 QY 1201 CAGGATCGAGGACATGAGGAAGCGGATGTCAGGTCTCCAGAGCCCTTTCGCCCCCGCG 1260
 DB |||||
 QY 1201 CAGGATCGAGGACATGAGGAAGCGGATGTCAGGTCTCCAGAGCCCTTTCGCCCCCGCG 1260
 DB |||||
 QY 1261 CCCTGCCTACCTCTCTCTCCCTGCGCTGCCAGAGGAGGAGGCCGCCCGAGGA 1320
 DB |||||
 QY 1261 CCCTGCCTACCTCTCTCTCCCTGCGCTGCCAGAGGAGGAGGCCGCCCGAGGA 1320
 DB |||||
 QY 1321 GCCACTGACTTCTGTCTGCCAAGTGCAGTATCAGGCCCTGTATGAGACACCTTGCA 1380
 DB |||||
 QY 1321 GCCACTGACTTCTGTCTGCCAAGTGCAGTATCAGGCCCTGTATGAGACACCTTGCA 1380
 DB |||||
 QY 1381 GATACATGTCAGGAGTGCATTGAGTAGGGCCGCGCAGTGCAGGCCCACTGCTGCCCGA 1440
 DB |||||
 QY 1381 GATACATGTCAGGAGTGCATTGAGTAGGGCCGCGCAGTGCAGGCCCACTGCTGCCCGA 1440
 DB |||||
 QY 1441 GGAAGTCCCGGAGCGGTGAGTCTGCGCTTTCCTCTCCGCTGCTAGCCAGGATGA 1500
 DB |||||
 QY 1441 GGAAGTCCCGGAGCGGTGAGTCTGCGCTTTCCTCTCCGCTGCTAGCCAGGATGA 1500
 DB |||||
 QY 1501 AGGGCTGGGTGCCCAACTGGGATGCCACTGGAGGCCACCCAGGAGCTGGCCGCGC 1560
 DB |||||
 QY 1501 AGGGCTGGGTGCCCAACTGGGATGCCACTGGAGGCCACCCAGGAGCTGGCCGCGC 1560
 DB |||||
 QY 1561 ACCTTACGCTTCAGCTGTGATCCGCTGCTCCCTCTTTTGGGTAGATGCGGCCCGGAT 1620
 DB |||||
 QY 1561 ACCTTACGCTTCAGCTGTGATCCGCTGCTCCCTCTTTTGGGTAGATGCGGCCCGGAT 1620
 DB |||||
 QY 1621 CAGGCTGACTCGCTGCTTTTGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
 DB |||||
 QY 1621 CAGGCTGACTCGCTGCTTTTGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
 DB |||||
 QY 1681 TAATCCCTCCCTCTTCTCCACCGGCACTGGGGAAGTCAAGAATGGGGCTTGGGGCTCT 1740
 DB |||||
 QY 1681 TAATCCCTCCCTCTTCTCCACCGGCACTGGGGAAGTCAAGAATGGGGCTTGGGGCTCT 1740
 DB |||||
 QY 1741 CAGGAGAACTGCTTCCCTGCGAGAGCTGGGTGGAGCTTCTTCTCCACCGGACACCG 1800
 DB |||||
 QY 1741 CAGGAGAACTGCTTCCCTGCGAGAGCTGGGTGGAGCTTCTTCTCCACCGGACACCG 1800
 DB |||||
 QY 1801 ACCCGCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
 DB |||||
 QY 1801 ACCCGCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
 DB |||||
 QY 1861 TTTTGGGCTGATGCTATTTCCTTTTGCAGCAGACCGAGTGTATTTAAACAGTCACTA 1920
 DB |||||
 QY 1861 TTTTGGGCTGATGCTATTTCCTTTTGCAGCAGACCGAGTGTATTTAAACAGTCACTA 1920
 DB |||||
 QY 1921 TTGATGGACATTTGGGTGTTTCCCATCTTTTGTGTTTACCATAAATAGGCAAGTAA 1980
 DB |||||
 QY 1921 TTGATGGACATTTGGGTGTTTCCCATCTTTTGTGTTTACCATAAATAGGCAAGTAA 1980
 DB |||||
 QY 1981 AAAAAAAAAAAAAA 1994
 DB |||||
 QY 1981 AAAAAAAAAAAAAA 1994
 DB |||||

RESULT 8
 ID AAA35028 standard; DNA; 8631 BP.
 AC AAA35028;
 DT 28-JUL-2000 (first entry)
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2717.
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytotatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 OS Homo sapiens.
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PF 03-AUG-1999; 99WO-US017712.
 PR 03-AUG-1998; 98US-0095212P.
 PA (UYEC-) UNIV EAST CAROLINA.
 PI Nyce JW;
 DR WPI; 2000-205971/18.
 PT New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.
 PS Disclosure; Page 969-971; 1343pp; English.
 CC The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytotatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing

Query Match 100.0%; Score 1994; DB 3; Length 8631;
 Best Local Similarity 100.0%; Pred. No. 0;

XX	Human low adenosine antisense oligonucleotide related sequence #2717.	QY	1	GGCAGAGCATGGCCCTTTGTGATCCAGGTGGGAAAATAAGGCCAGAGAAAGTGAGGACC	60
DE		Db	6638	GGCAGAGCATGGCCCTTTGTGATCCAGGTGGGAAAATAAGGCCAGAGAAAGTGAGGACC	6697
XX	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;	QY	61	CGCGAGATATCAATCCAGTCTCTTCCCTCACTCCCTGTGAAGCTCTCCAGCATCATC	120
KW	human; airway disorder; bronchoconstriction; lung inflammation;	Db	6698	CGCGAGATATCAATCCAGTCTCTTCCCTCACTCCCTGTGAAGCTCTCCAGCATCATC	6757
KW	surfactant depletion; respiratory bronchodilator; antiinflammatory;	QY	121	GAGGTCCCATCAGCCCTTGGCCCTTTGGATGAATAGGACCTCTGAGAGAGCCAACTGTG	180
KW	immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosolic;	Db	6758	GAGGTCCCATCAGCCCTTGGCCCTTTGGATGAATAGGACCTCTGAGAGAGCCAACTGTG	6817
KW	respiratory obstruction; pulmonary obstruction; impeded respiration;	QY	181	TCAGATGCTGACGCCAGTGGTGGCCCGGACAGCATCAGGACGTACTCGGCGAAGAGTC	240
KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;	Db	6818	TCAGATGCTGACGCCAGTGGTGGCCCGGACAGCATCAGGACGTACTCGGCGAAGAGTC	6877
KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;	QY	241	TCCTCTGGGGAAGCCAGCCATGCTGCACTCTGCTTTCAGAAACAGGGCGCTCTTGAGACCT	300
KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;	Db	6878	TCCTCTGGGGAAGCCAGCCATGCTGCACTCTGCTTTCAGAAACAGGGCGCTCTTGAGACCT	6937
KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;	QY	301	CCAGCGCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGCAGAGCAACAGAT	360
XX	Canis sapiens.	Db	6938	CCAGCGCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGCAGAGCAACAGAT	6997
XX	WO200062736-A2.	QY	361	TCGCGGAGCGCTGCGAGGAGCTTCTGCATTTTCAAGCCAGCAGAGAGGAGGAAGA	420
XX	26-OCT-2000.	Db	6998	TCGCGGAGCGCTGCGAGGAGCTTCTGCATTTTCAAGCCAGCAGAGGAGGAAGA	7057
XX	24-MAR-2000; 2000WO-US008020.	QY	421	GTTCTCATGTGCAAGTTCCAGGAGGCCAGGAAACTGTGTGAGAGACTCGGCTCGAGAA	480
XX	06-APR-1999; 99US-0127958P.	Db	7058	GTTCTCATGTGCAAGTTCCAGGAGGCCAGGAAACTGTGTGAGAGACTCGGCTCGAGAA	7117
XX	(UYEC-) UNIV EAST CAROLINA.	QY	481	GCTCGATCTGAAGGCGCAGAGGAGCAGGCTCTGCGGAGGCTGGAGCACTCAAGAGATG	540
PA	(NYCE/) NYCE J W.	Db	7118	GCTCGATCTGAAGGCGCAGAGGAGCAGGCTCTGCGGAGGCTGGAGCACTCAAGAGATG	7177
XX	Nyce JW;	QY	541	CCAGCAGCAGATGGCTGAGGACCAAGGCTCTGTGAAAGCCAGGTGAGCTCTTGTCTGG	600
DR	WPI; 2000-679539/66.	Db	7178	CCAGCAGCAGATGGCTGAGGACCAAGGCTCTGTGAAAGCCAGGTGAGCTCTTGTCTGG	7237
XX	Low adenosine (A) content antisense oligonucleotides which do not trigger	QY	601	GGAGCTGCGAGAGCCAGAGTCTGTGGAGCTGCCACTAAGGAATGCAAGCTCTTGA	660
PT	adenosine receptors during metabolism, useful e.g. for treating cancers	Db	7238	GGAGCTGCGAGAGCCAGAGTCTGTGGAGCTGCCACTAAGGAATGCAAGCTCTTGA	7297
PT	and respiratory obstructions.	QY	661	GGGTCCGCGCCGCGCGCCAGGAGCAGCGCGGCGAGCTGGAGAGTGAGCGCGAGCGCT	720
XX	Disclosure; Page 1046-1048; 1592pp; English.	Db	7298	GGGTCCGCGCCGCGCGCCAGGAGCAGCGCGGCGAGCTGGAGAGTGAGCGCGAGCGCT	7357
CC	The present invention describes low adenosine (A) content antisense	QY	721	GCAGCAGCAGCAGCAGCTGCGAGTGGACCCAGCTGCGCATGCGAGGCGCAGAGCTGGAGGC	780
CC	oligonucleotides and compositions (I) comprising them. In the antisense	Db	7358	GCAGCAGCAGCAGCAGCTGCGAGTGGACCCAGCTGCGCATGCGAGGCGCAGAGCTGGAGGC	7417
CC	oligonucleotides the A is replaced by a 'universal' or alternative base.	QY	781	CGCGTCTCGCATGAGAGCCAGGCGCTCTCGAGAGAGAGAGAAAGCTGGCCAGTTGCA	840
CC	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,	Db	7418	CGCGTCTCGCATGAGAGCCAGGCGCTCTCGAGAGAGAGAGAAAGCTGGCCAGTTGCA	7477
CC	immunosuppressive, antiasthmatic, hypotensive and cytosolic activities.	QY	841	GGTGGCTTATCAGCAGCTCTTCCAGAGATAGCAGAACCCACATCAAGAGCAGCGTGGTGG	900
CC	The antisense oligonucleotides and (I) can be used to down-regulate the	Db	7478	GGTGGCTTATCAGCAGCTCTTCCAGAGATAGCAGAACCCACATCAAGAGCAGCGTGGTGG	7537
CC	expression and/or activity of target polypeptides associated with	QY	901	CAGTGAGCGGAAGCAGGAGAAATGCAAGTCTCAAAACAGAGCAGCTCCAGAGCGCGA	960
CC	lung/respiratory disorders and malignancies, such as stimulating and	Db	7538	CAGTGAGCGGAAGCAGGAGAAATGCAAGTCTCAAAACAGAGCAGCTCCAGAGCGCGA	7597
CC	activating peptide factors and transmitters, transcription factors,	QY	961	GGAGGCCCTGTGTGGCCAAACAGGAGGTGATCGATGAAGCTGAAGAGAGAGGCGCGAGCA	1020
CC	immunoglobulins and antibodies, antibody receptors, cytokines and	Db	7598	GGAGGCCCTGTGTGGCCAAACAGGAGGTGATCGATGAAGCTGAAGAGAGAGGCGCGAGCA	7657
CC	chemokines, endogenously produced specific and non-specific enzymes,	QY	1021	CAAGATTGTTGAGAGCCGTTCCGTTGCTGAAGCCCGAGCGGATATCTCAAGCGCGA	1080
CC	binding proteins, adhesion molecules and their receptors, cytokine and	Db	7658	CAAGATTGTTGAGAGCCGTTCCGTTGCTGAAGCCCGAGCGGATATCTCAAGCGCGA	7717
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central	QY	1081	CTTCCAGGCTGAGAGGCGCGGAGAGAGCTGGCCGAGAGAGAGGAGCTCTCTGAGGA	1140
CC	nervous system (CNS) and peripheral nervous and non-nervous system				
CC	receptors, CNS and peripheral nervous and non-nervous system peptide				
CC	transmitters, defensins, growth factors, vasoactive peptides and				
CC	receptors, binding proteins and malignancy associated proteins. The				
CC	antisense oligonucleotides may be used in this way to treat disorders				
CC	including respiratory obstruction (especially pulmonary obstruction				
CC	and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or				
CC	surfactant hypoproduction which are associated with a disease or				
CC	condition selected from pulmonary vasoconstriction, inflammation,				
CC	allergies, asthma, impeded respiration, respiratory distress syndrome				
CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary				
CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),				
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,				
CC	and/or cancer. AAF18434 to AAF21543 represent human polynucleotide				
CC	fragments and antisense oligonucleotides used in the exemplification of				
CC	the present invention				
XX	Sequence 8631 BP; 2280 A; 2050 C; 2270 G; 2031 T; 0 U; 0 Other;				
SQL	Query Match 100.0%; Score 1994; DB 3; Length 8631;				
	Best Local Similarity 100.0%; Pred. No. 0;				
	Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

Db 6818 TGAGATGGTGCAGCCCAAGTGGTGGCCCGCAGCAGATCAGGACGTACTGGGCGAAGAGTC 6877
Qy 241 TCCTCTGGGGAAGCCAGCCATGCTGCACCTGCTTCAGAACAGGGCGCTCCCTGAGACCTT 300
Db 6878 TCCTCTGGGGAAGCCAGCCATGCTGCACCTGCTTCAGAACAGGGCGCTCCCTGAGACCTT 6937
Qy 301 CCAGCGCTCCCTGGAGGAGAATCAAGAGCTCCGAGATGCTCCGCGCAGAGCAACCCAGAT 360
Db 6938 CCAGCGCTCCCTGGAGGAGAATCAAGAGCTCCGAGATGCTCCGCGCAGAGCAACCCAGAT 6997
Qy 361 TCTGCGGAGCGCTGCGAGAGCTTCTGCATTTCAAGCAGCAGCAGAGGAGAGAGGA 420
Db 6998 TCTGCGGAGCGCTGCGAGAGCTTCTGCATTTCAAGCAGCAGCAGAGGAGAGAGGA 7057
Qy 421 GTTCTCTCATGTGCAAGTTCCAGAGAGCCAGGAAACTGTGTGGAGAGACTCGGCTTGAGAA 480
Db 7058 GTTCTCTCATGTGCAAGTTCCAGAGAGCCAGGAAACTGTGTGGAGAGACTCGGCTTGAGAA 7117
Qy 481 GCTCGATCTGAAGAGSCAGAAGCAGAGCTCTGCGGAGGTGGAGCACTTGAAGAGATG 540
Db 7118 GCTCGATCTGAAGAGSCAGAAGCAGAGCTCTGCGGAGGTGGAGCACTTGAAGAGATG 7177
Qy 541 CCAGCAGCAGATGGCTGAGGAACAAGCCCTCTGTGAAGCCCAAGGTGAACCTCTTGTCTGG 600
Db 7178 CCAGCAGCAGATGGCTGAGGAACAAGCCCTCTGTGAAGCCCAAGGTGAACCTCTTGTCTGG 7237
Qy 601 GGAGCTGCAAGGAGAGCCAGAGTCGCTTGGAGGCTGCCACTAAGGAATGCGAGCTCTGGA 660
Db 7238 GGAGCTGCAAGGAGAGCCAGAGTCGCTTGGAGGCTGCCACTAAGGAATGCGAGCTCTGGA 7297
Qy 661 GGGTCCGGGCCCGGGCCAGCAGCAGCGCGGCGAGCTGGAGAGTGAAGCGAGCGCGCT 720
Db 7298 GGGTCCGGGCCCGGGCCAGCAGCAGCGCGGCGAGCTGGAGAGTGAAGCGAGCGCGCT 7357
Qy 721 GCAGCAGCAGCAGCGCTGAGTGACAGCTGCGCATGCAAGGCGCAGAGCGTGGAGGC 780
Db 7358 GCAGCAGCAGCAGCGCTGAGTGACAGCTGCGCATGCAAGGCGCAGAGCGTGGAGGC 7417
Qy 781 CCGCTTCCGATGAGCGCCAGCGCCCTCGAGAGAGAGAGAGCTGGCCAGCTTGA 840
Db 7418 CCGCTTCCGATGAGCGCCAGCGCCCTCGAGAGAGAGAGAGCTGGCCAGCTTGA 7477
Qy 841 GGTGGCCTATCACCAGCTCTTCAAGAAATACGACCAACCAATCAAGAGCAGCGTGGTGG 900
Db 7478 GGTGGCCTATCACCAGCTCTTCAAGAAATACGACCAACCAATCAAGAGCAGCGTGGTGG 7537
Qy 901 CAGTGAAGCGAAGCGAGGAATGAGCTGGAAGATCTCAAAACAGCAGCTCCAGAGGCCGA 960
Db 7538 CAGTGAAGCGAAGCGAGGAATGAGCTGGAAGATCTCAAAACAGCAGCTCCAGAGGCCGA 7597
Qy 961 GGAGGCCCTGGTGGCCAAACAGAGAGTGCATAGCTGAGAGGAGGAGGCCGAGCAGCA 1020
Db 7598 GGAGGCCCTGGTGGCCAAACAGAGAGTGCATAGCTGAGAGGAGGAGGCCGAGCAGCA 7657
Qy 1021 CAAGATTGTGTGAGAGCCGCTTCCGCTGCTGAAGCCCAAGCGCGATATCTCAAGGCGGA 1080
Db 7658 CAAGATTGTGTGAGAGCCGCTTCCGCTGCTGAAGCCCAAGCGCGATATCTCAAGGCGGA 7717
Qy 1081 CTTTCAGGCTGAGAGCGCAGCGCCGGGAGAAAGTGGCCGAGAGAGAGAGCTCTTGCAGGA 1140
Db 7718 CTTTCAGGCTGAGAGCGCAGCGCCGGGAGAAAGTGGCCGAGAGAGAGAGCTCTTGCAGGA 7777
Qy 1141 GCAGCTGGAGCAGCTGCGAGAGGAGTACAGCAAACTGAGGCCAGCTGTTCAGAGTCCGC 1200
Db 7778 GCAGCTGGAGCAGCTGCGAGAGGAGTACAGCAAACTGAGGCCAGCTGTTCAGAGTCCGC 7837
Qy 1201 CAGGATTCAGAGCAGATGAGGAAGCGGATGTCAGAGTCTCCAGGCCCTTCCGCCCCCGC 1260
Db 7838 CAGGATTCAGAGCAGATGAGGAAGCGGATGTCAGAGTCTCCAGGCCCTTCCGCCCCCGC 7897
Qy 1261 CCTCTGCTACCT 1320
Db 7898 CCTCTGCTACCT 7957

Qy 1321 GCCACCTGACTTCTGCTGTGCCAAGTGCAGTATCAGGCCCCCTGATATATGACACCCCTGCA 1380
Db 7958 GCCACCTGACTTCTGCTGTGCCAAGTGCAGTATCAGGCCCCCTGATATATGACACCCCTGCA 8017
Qy 1381 GATACATGTCATGGAGTGCATTGAGTAGGGCCGGCCAGTGCAGAGGCACTTGCCTGCCGA 1440
Db 8018 GATACATGTCATGGAGTGCATTGAGTAGGGCCGGCCAGTGCAGAGGCACTTGCCTGCCGA 8077
Qy 1441 GGAAGTGGCCGGGACCGTGCAGTCTGCGCTTTCCTCTCCGGCTGCTAGCCAGGATGA 1500
Db 8078 GGAAGTGGCCGGGACCGTGCAGTCTGCGCTTTCCTCTCCGGCTGCTAGCCAGGATGA 8137
Qy 1501 AGGGCTGGGTGGCCCAACTGGGATGCCACTGGAGCCCCACCAGGAGCTGCGCGCGGC 1560
Db 8138 AGGGCTGGGTGGCCCAACTGGGATGCCACTGGAGCCCCACCAGGAGCTGCGCGCGGC 8197
Qy 1561 ACCTTACGCTTCAGCTGTGATCCGCTGCTCCCTCTTTTGGGGTAGATGCGGCCCCCGAT 1620
Db 8198 ACCTTACGCTTCAGCTGTGATCCGCTGCTCCCTCTTTTGGGGTAGATGCGGCCCCCGAT 8257
Qy 1621 CAGGCTGACTGCTGCTCTTTTGGTTCCTTCTGTCTGCTCGAACCACTTGCCTCGGGC 1680
Db 8258 CAGGCTGACTGCTGCTCTTTTGGTTCCTTCTGTCTGCTCGAACCACTTGCCTCGGGC 8317
Qy 1681 TAATCCCTCCCTCTTCCACCCGCACTGGGGAAGTCAAGAAATGGGGCTTGGGGCTCT 1740
Db 8318 TAATCCCTCCCTCTTCCACCCGCACTGGGGAAGTCAAGAAATGGGGCTTGGGGCTCT 8377
Qy 1741 CAGGAGAACTGCTTCCCTTCCCTGGCAGAGCTGGGTGGCAGCTTTCCTCCACCGGACACCG 1800
Db 8378 CAGGAGAACTGCTTCCCTTCCCTGGCAGAGCTGGGTGGCAGCTTTCCTCCACCGGACACCG 8437
Qy 1801 ACCGCCCGCGCTGCTGCGCTGGGAGTGTGCCCTTCTTACATGACACAGGCTGCTCTCC 1860
Db 8438 ACCGCCCGCGCTGCTGCGCTGGGAGTGTGCCCTTCTTACATGACACAGGCTGCTCTCC 8497
Qy 1861 TTTTGGGCTGCATGCTATTTCATTTTGACGCGAGACCGATGTATTTAAACAGTCACTA 1920
Db 8498 TTTTGGGCTGCATGCTATTTCATTTTGACGCGAGACCGATGTATTTAAACAGTCACTA 9557
Qy 1921 TTGATGGACATTTGGTGTGTTTCCCATCTTTTGTATCCATAAATAATAGGATAGTAAAA 1980
Db 8558 TTGATGGACATTTGGTGTGTTTCCCATCTTTTGTATCCATAAATAATAGGATAGTAAAA 8617
Qy 1981 AAAAAAAAAAAAAA 1994
Db 8618 AAAAAAAAAAAAAA 8631

RESULT 11
ABD20693
ID ABD20693 standard; DNA; 8631 BP.
XX
AC ABD20693;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human pulmonary and inflammatory target DNA #304.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antisthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
OS Homo sapiens.
XX
PN WO200285309-A2.
XX

PD	31-OCT-2002.	
XX		
PF	23-APR-2002; 2002WO-US013143.	
XX		
PR	24-APR-2001; 2001US-0286036P.	
XX		
PA	(EPIG-) EPIGENESIS PHARM INC.	
XX		
PI	Nyco JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;	
PI	Miller S, Tang L, Shahabuddin S;	
XX		
DR	WPI; 2003-093058/08.	
XX		
PT	Pharmaceutical composition for treating asthma, has antisense	
PT	oligonucleotide containing less percentage of adenosine, targeted to	
PT	nucleic acids associated with lung airway or lung dysfunction, and	
XX	bronchodilating agent.	
XX		
PS	Claim 15; SEQ ID NO 12086; 763pp; English.	
XX		
CC	This invention describes a novel composition (a) a first active agent,	
CC	comprising oligonucleotides, effective for alleviating	
CC	bronchoconstriction, respiratory tract inflammation, allergies and	
CC	reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,	
CC	surfactant depletion or hyposecretion, when administered to a mammal. The	
CC	oligonucleotides are derived from a gene encoding or regulating	
CC	expression of a target polypeptide associated with lung airway or lung	
CC	dysfunction or cancer and can be anti-sense to the corresponding mRNA.	
CC	The invention also describes a kit, that comprises: (a) a delivery	
CC	device, in separate containers, (b) the oligonucleotides, (c)	
CC	instructions for adding a carrier and for use of the kit. The composition	
CC	of the invention has anti-allergic, anti-inflammatory, antiasthmatic,	
CC	analgesic, hypotensive, immunosuppressive and cytostatic activity, is a	
CC	beta-adrenergic agonist. The composition is useful for preventing or	
CC	treating a respiratory, lung or malignant disease. The administered	
CC	composition comprises oligo and is administered to reduce the production	
CC	or availability, or to increase the degradation of the target mRNA or to	
CC	reduce the amount of target polypeptide present in the lungs. The	
CC	pulmonary obstruction, and/or bronchoconstriction and/or lung	
CC	inflammation, allergies and/or surfactant hypoproduction are associated	
CC	with a disease or condition such as pulmonary vasoconstriction,	
CC	inflammation, allergies, asthma, impeded respiration, respiratory	
CC	distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary	
CC	hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary	
CC	transplantation rejection, pulmonary infections, bronchitis or cancer.	
CC	The reduced adenosine content of the anti-sense oligos corresponding to	
CC	thymidines present in the target RNA serves to prevent the breakdown of	
CC	the oligonucleotides into products that free adenosine into the system	
CC	e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to	
XX	prevent any unwanted effects due to it	
XX		
SQ	Sequence 8631 BP; 2280 A; 2051 C; 2270 G; 2030 T; 0 U; 0 Other;	
	Query Match 99.9%; Score 1992.4; DB 11; Length 8631;	
	Best Local Similarity 99.9%; Pred. No. 0;	
	Matches 1993; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 GCACGACGATCGCCCTTGATCTCAGGTGGGAAACTAAGGCCAGAGAAGTGGAGCC 60	
Db	6638 GCACGACGATCGCCCTTGATCTCAGGTGGGAAACTAAGGCCAGAGAAGTGGAGCC 6637	
QY	61 CGCAGACGATCAATCCAGTCTCTTCCCTCACTCCCTGTCAAGCTCTCCAGGATCATC 120	
Db	6698 CGCAGACGATCAATCCAGTCTCTTCCCTCACTCCCTGTCAAGCTCTCCAGGATCATC 6757	
QY	121 GAGGTCCCATCAGCCCTTGCCCTTGTTGGATGAATAGGCACCTCTCGAAGAGCCAACTGTG 180	
Db	6758 GAGGTCCCATCAGCCCTTGCCCTTGTTGGATGAATAGGCACCTCTCGAAGAGCCAACTGTG 6817	
QY	181 TGAGATGGTGAGCCGACGAGTGGTGGCCGCGCAGCAGATCAGGACGTACTCTGGCGAGAGTGC 240	
Db	6818 TGAGATGGTGAGCCGACGAGTGGTGGCCGCGCAGCAGATCAGGACGTACTCTGGCGAGAGTGC 6877	

Db 7958 GGCACCTGACTTCTGCTGCCAAGTGCAGTATCAGGCCCTGTATGACACCCCTGCA 8017
Qy 1381 GATACATGTCATGAGTGCATTGAGTAGGGCCGCGCAGTGCAAGGCCACTGCTGCCCGA 1440
Db 8018 GATACATGTCATGAGTGCATTGAGTAGGGCCGCGCAGTGCAAGGCCACTGCTGCCCGA 8077
Qy 1441 GGAAGTCCCGGACCGTGCAGTCTGCGCTTTCTCTCCCGCTGCTAGCCAGGATGA 1500
Db 8078 GGAAGTCCCGGACCGTGCAGTCTGCGCTTTCTCTCCCGCTGCTAGCCAGGATGA 8137
Qy 1501 AGGGCTGGGTGGCCACAACCTGGATGCCACCTGGAGCCGCCACCCAGGAGTGGCCCGGC 1560
Db 8138 AGGGCTGGGTGGCCACAACCTGGATGCCACCTGGAGCCGCCACCCAGGAGTGGCCCGGC 8197
Qy 1561 ACCTTACGCTTACGCTTGGATCCGCTGGTCCCTCTTTTGGGTAGATGGCCCGCAT 1620
Db 8198 ACCTTACGCTTACGCTTGGATCCGCTGGTCCCTCTTTTGGGTAGATGGCCCGCAT 8257
Qy 1621 CAGGCTGACTCGTCTCTTTTGTTCCTTCTGCTCGAACCACTTGGCTCGGGC 1680
Db 8258 CAGGCTGACTCGTCTCTTTTGTTCCTTCTGCTCGAACCACTTGGCTCGGGC 8317
Qy 1681 TAATCCTCCTCTTCTCCACCCGCACTGGGGAAGTCAAGAAATGGGCTTGGGCTCT 1740
Db 8318 TAATCCTCCTCTTCTCCACCCGCACTGGGGAAGTCAAGAAATGGGCTTGGGCTCT 8377
Qy 1741 CAGGGAAGTCTTCCCTGGCAGAGTGGGTGGGAGTCTTCTCCACCGGACACG 1800
Db 8378 CAGGGAAGTCTTCCCTGGCAGAGTGGGTGGGAGTCTTCTCCACCGGACACG 8437
Qy 1801 ACCCGCCGCGCTGTGCTGGAGTGTGCTTACCATGACACGGGTGCTCTCC 1860
Db 8438 ACCCGCCGCGCTGTGCTGGAGTGTGCTTACCATGACACGGGTGCTCTCC 8497
Qy 1861 TTTTGGGCTGCATGCTTATTCATTTTTCAGCCAGACCGATGTATTTAACCAAGTCACTA 1920
Db 8498 TTTTGGGCTGCATGCTTATTCATTTTTCAGCCAGACCGATGTATTTAACCAAGTCACTA 8557
Qy 1921 TTGATGCAATTTGGGTGTTTCCCATCTTTTGGTACCAATAAATGGCATAGTAA 1980
Db 8558 TTGATGCAATTTGGGTGTTTCCCATCTTTTGGTACCAATAAATGGCATAGTAA 8617
Qy 1981 AAAAAAAAAAAAAA 1994
Db 8618 AAAAAAAAAAAAAA 8631
RESULT 12
ADQ87415
XX ADQ87415 standard; cDNA; 1967 BP.
AC ADQ87415;
XX
XX
DT 07-OCT-2004 (first entry)
XX Human tumour-associated antigenic target (TAT) cDNA sequence #4292.
DE human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
XX Homo sapiens.
XX WO2004060270-A2.
PN
XX
XX 22-JUL-2004.
PD
XX
XX 15-OCT-2003; 2003WO-US029126.
PF
XX
XX 18-OCT-2002; 2002US-0418988P.
PR
XX
XX (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA

(ZHOU/) ZHOU Y.
Wu TD, Zhou Y;
WPI; 2004-534300/51.
New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
Claim 1; SEQ ID NO 4292; 5504pp; English.
The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.
Sequence 1967 BP; 409 A; 581 C; 629 G; 348 T; 0 U; 0 Other;
Query Match 98.0%; Score 1954.4; DB 13; Length 1967;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1966; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 9 CATGCCCTTGTGATCCAGGTGGGNAACTAGGCCCCAGAGAGTCCAGACCCCGCAGAC 68
Db 1 CATGCCCTTGTGATCCAGGTGGGNAACTAGGCCCCAGAGAGTCCAGACCCCGCAGAC 60
Qy 69 TATCAATCCAGTCTCTTCCCTCACTCCCTGTGAAGTCTCCAGCATCATCGAGTCCC 128
Db 61 TATCAATCCAGTCTCTTCCCTCACTCCCTGTGAAGTCTCCAGCATCATCGAGTCCC 120
Qy 129 ATCAGCCCTTGGCTTGTGGATGAATAGCACTCTGGAAAGAGCCCACTGTGTGAGATGG 188
Db 121 ATCAGCCCTTGGCTTGTGGATGAATAGCACTCTGGAAAGAGCCCACTGTGTGAGATGG 180
Qy 189 TGCAGCCAGTGGTGGCCCGGAGCAGATCAGAGTACTTGGCGGAGAGTCTCTCTGG 248
Db 181 TGCAGCCAGTGGTGGCCCGGAGCAGATCAGAGTACTTGGCGGAGAGTCTCTCTGG 240
Qy 249 GGAAGCCAGCCATGCTGCACCTGCTTCAGAACAGGGCGCTCTCTGAGACCTCCAGCGCT 308

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) - (c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

Sequence 1967 BP; 409 A; 591 C; 629 G; 348 T; 0 U; 0 Other;

Query	March	98.0%;	Score	1954.4;	DB	13;	Length	1967;
Best Local	Similarity	99.9%;	Pred.	No. 0;				
Matches	1966;	Conservative	0;	Mismatches	1;	Indels	1;	Gaps
Qy	9	CATGGCCCTTGTATCCAGGTGGGAAACTAAGGCCCCAGAGAAGTGAGACCCCGCAGAC	68					
Db	1	CATGGCCCTTGTATCCAGGTGGGAAACTAAGGCCCCAGAGAAGTGAGACCCCGCAGAC	60					
Qy	69	TATCAATCCCAAGTCTCTTCCCTCTCACTCCCTGTGAAGCTCTCCAGCATCATCGAGTCCC	128					
Db	61	TATCAATCCCAAGTCTCTTCCCTCTCACTCCCTGTGAAGCTCTCCAGCATCATCGAGTCCC	120					
Qy	129	ATCAGCCCTTGCCTCTGTTGGATGAATAGGACACTCTGGAAAGAGCCAACTGTGTGAGATGG	188					
Db	121	ATCAGCCCTTGCCTCTGTTGGATGAATAGGACACTCTGGAAAGAGCCAACTGTGTGAGATGG	180					
Qy	189	TGCAGCCCAAGTGTGGCCCGCAGCAGATCAGGAGCTACTGGCGGAAGAGTCTCCTCTGG	248					
Db	181	TGCAGCCCAAGTGTGGCCCGCAGCAGATCAGGAGCTACTGGCGGAAGAGTCTCCTCTGG	240					
Qy	249	GGAAAGCCAGCCATGCTGCACCTGCCTTCAGAACAGGGCGCTCTTGAGACCCCTCCAGCGCT	308					
Db	241	GGAAAGCCAGCCATGCTGCACCTGCCTTCAGAACAGGGCGCTCTTGAGACCCCTCCAGCGCT	300					
Qy	309	GCCTTGGAGGAGAACTCAAGAGCTCCGAGATGCCATCCCGCAGAGCAACAGATTCTGCGGG	368					

QY 1449 CCGGACCGTGCAGTCTGCGCTTTCTCTCTCCCGCTGCTAGCCACGAGTGAAGGGCTGG 1508
DB 1440 CCGGACCGTGCAGTCTGCGCTTTCTCTCTCCCGCTGCTAGCCACGAGTGAAGGGCTGG 1499
QY 1509 GTGGCCCAACTGGGATGCGGCTGAGGAGCCACCCAGGAGTGGCGGGGACCTTACG 1568
DB 1500 GTGGCCCAACTGGGATGCGGCTGAGGAGCCACCCAGGAGTGGCGGGGACCTTACG 1559
QY 1569 CTTGAGCTGTATGCGCTGGTCCCTCTTTTGGGATAGATCGGCGCCCGATCAGGCTTG 1628
DB 1560 CTTGAGCTGTATGCGCTGGTCCCTCTTTTGGGATAGATCGGCGCCCGATCAGGCTTG 1619
QY 1629 ACTGCTGTCTTTTGTCT 1688
DB 1620 ACTGCTGTCTTTTGTCT 1679
QY 1689 CCTCTTCTCCACCCCGCACTGGGGAAGTCAAGATGGGGCTCTCTCAGGAGAGA 1748
DB 1680 CCTCTTCTCCACCCCGCACTGGGGAAGTCAAGATGGGGCTCTCTCAGGAGAGA 1739
QY 1749 ACTGCTTCCCTGGCAGCTGGTGGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1808
DB 1740 ACTGCTTCCCTGGCAGCTGGTGGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1799
QY 1809 GCGCTGTGCTTGGGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1868
DB 1800 GCTGTGTGCTTGGGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1859
QY 1869 TGCATGTATTCATTTTGCAGCAGCAGTGTGTATTTAACCACTCACTATTGATGGA 1928
DB 1860 TGCATGTATTCATTTTGCAGCAGCAGTGTGTATTTAACCACTCACTATTGATGGA 1919
QY 1929 CATTGGGTGTTTCCCATCTTTTGTACCAATAAATATGTCATAGT 1976
DB 1920 CATTGGGTGTTTCCCATCTTTTGTACCAATAAATATGTCATAGT 1967

RESULT 14

ACD23012
ID ACD23012 standard; cDNA; 2035 BP.

XX ACD23012;

XX 25-AUG-2003 (first entry)

XX Human NEMO cDNA.

XX Human; gene; 85; NF-kappaB essential modulator; nuclear factor kappa B;
XX incontinentia pigmenti; X-linked disorder; chromosome Xq28; NEMO;
XX immunomodulatory; dermatological; osteopathic; neuropathic;
XX apoptosis-related disease; immune-system related disease;
XX blood vessel-related disease; skin defect; dental defect; osteopetrosis;
XX ophthalmologic defect; neurological defect.

OS Homo sapiens.

XX US200302055-A1.

XX 13-FEB-2003.

XX 22-MAY-2001; 2001US-00863049.

XX 22-MAY-2000; 2000US-0206223P.

XX (KENW/) KENNRICK S. J.

XX (WOF/) WOFFENDIN H.

XX (MUN/) MUNNICH A.

XX (SMH/) SMAHI A.

XX (ISRA/) ISRAEL A.

XX (POUS/) POUSTRKA A.

XX (HEIS/) HEISS N.

XX (DURS/) D'URSO M.

PA (LEWI/) LEWIS R. A.
PA (NELS/) NELSON D. L.
PA (ARAD/) ARADHYA S.
PA (LEVY/) LEVY M.

XX Kenrick SJ, Woffendin H, Munnich A, Smahi A, Israel A;
PI Poustka A, Heiss N, D'urso M, Lewis RA, Nelson DL, Aradhy S;
PI Levy M;

XX WPI: 2003-492063/46.

XX P-PSDB; ABO17485.

XX Detection of necrosis factor-kappa B related medical condition in
PT organism, by obtaining sample from the organism, and analyzing the sample
PT for alteration in specified amino acid sequences.

PS Disclosure; Page; 44pp; English.

XX The invention relates to a nuclear factor-kappa B (NF-kappa B) related
CC medical condition in an organism being detected by obtaining a sample
CC from the organism, and analysing the sample for an alteration in a the
CC nuclear factor kappaB essential modifier (NEMO) gene or protein sequence
CC (neither shown in the specification). The alteration results in
CC inactivation of NF-kappa B. Also included are treating or preventing NF-
CC kappa B related medical condition in an organism by administering the
CC NEMO protein to the organism and screening a test organism for a compound
CC for the treatment of NF-kappa B related medical condition (by
CC administering the compound to the organism, and assaying for an
CC improvement in the NF-kappa B related medical condition). The method
CC useful is for detecting NF-kappa B related condition, e.g. incontinentia
CC pigmenti (IP), apoptosis-related disease, immune-system related disease,
CC blood vessel-related disease, skin defect, dental defect, osteopetrosis,
CC ophthalmologic defect, or neurological defect, in an organism, i.e. human
CC individual. The NEMO gene is located on chromosome Xq28, incontinentia
CC pigmenti being an X-linked disorder. Experiments in this study show
CC variations in exon 2, 10, 9 and particularly intron 3 to be linked to
CC familial incontinentia pigmenti. The present sequence is the human NEMO
CC cDNA. Note: The present sequence is not shown in the specification but
CC was obtained from Genbank using the reference number given in the
CC specification

XX SQ Sequence 2035 BP; 425 A; 592 C; 637 G; 381 T; 0 U; 0 Other;

Query Match 92.1%; Score 1836.4; DB 9; Length 2035;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1848; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 132 AGCCCTTGCCCTGTTGGATGAATAGCACCTCTGGAAGAGCCCACTGTGAGATGTTGC 191

DB 169 AGCCCTTGCCCTGTTGGATGAATAGCACCTCTGGAAGAGCCCACTGTGAGATGTTGC 228

QY 192 AGCCCAAGTGTGTCGCCCGGAGCAGATCAGACGCTACTGGGCGAAGAGTCTCTCTTGGGGA 251

DB 229 AGCCCAAGTGTGTCGCCCGGAGCAGATCAGACGCTACTGGGCGAAGAGTCTCTCTTGGGGA 288

QY 252 AGCCACGATGTCGACCTGCTTCAAGACAGGCGCTCTGAGACCTCCAGGCTGCC 311

DB 289 AGCCACGATGTCGACCTGCTTCAAGACAGGCGCTCTGAGACCTCCAGGCTGCC 348

QY 312 TGGAGGAGAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCAAGATTCTCGGGAGC 371

DB 349 TGGAGGAGAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCAAGATTCTCGGGAGC 408

QY 372 GCTGCGAGGAGCTTCTGCAATTTCCAAAGCCAGCAGAGGAGGAGAGGAGTCTCTCATGT 431

DB 409 GCTGCGAGGAGCTTCTGCAATTTCCAAAGCCAGCAGAGGAGGAGAGGAGTCTCTCATGT 468

QY 432 GCAAGTTTCCAGGAGGCCAGGAACTGGTGGAGAGACTCGSCCTGGAGAGCTCGATCTGA 491

DB 469 GCAAGTTTCCAGGAGGCCAGGAACTGGTGGAGAGACTCGSCCTGGAGAGCTCGATCTGA 528

QY 492 AGAGGCAGAAAGGAGCAGGCTCTGCGGGAGGTGGACCTGAAGAGATGCCAGCAGAGA 551

Db 529 AGAGGAGAGGAGGAGGCTCTCGGGAGGTGGAGCACTGAAGAGATGCCAGCAGCAGA 588
QY 552 TGGCTGAGACAAAGGCTCTGTGAAGCCAGGTGACGTCTTGTCTGGGGAGCTGCGAG 611
Db 589 TGGCTGAGACAAAGGCTCTGTGAAGCCAGGTGACGTCTTGTCTGGGGAGCTGCGAG 648
QY 612 AGAGCCAGAGTCCGTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGGTCCGGGCC 671
Db 649 AGAGCCAGAGTCCGTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGGTCCGGGCC 708
QY 672 GGGCGGCCAGCAGCAGCGCGCCAGCTGGAGAGTGAAGCCAGGCGCTGTCAGCAGCAGC 731
Db 709 GGGCGGCCAGCAGCAGCGCGCCAGCTGGAGAGTGAAGCCAGGCGCTGTCAGCAGCAGC 768
QY 732 ACAGCGTCAGAGTGACACGCTGCCATGCGAGCCAGGCGCAGAGCGCTGAGGCGCGCTCCGCA 791
Db 769 ACAGCGTCAGAGTGACACGCTGCCATGCGAGCCAGGCGCAGAGCGCTGAGGCGCGCTCCGCA 828
QY 792 TGGAGCGCCAGGCGCGCTCGAGGAGGAAGAGGAAGCTGGCCAGTTGCAAGTGGGCTATC 851
Db 829 TGGAGCGCCAGGCGCGCTCGAGGAGGAAGAGGAAGCTGGCCAGTTGCAAGTGGGCTATC 888
QY 852 ACCAGCTCTTCCAAGAATACGCAACCAACATCAAGAGCAGCGTGGTGGGCACTGAGCGGA 911
Db 889 ACCAGCTCTTCCAAGAATACGCAACCAACATCAAGAGCAGCGTGGTGGGCACTGAGCGGA 948
QY 912 AGCGAGGAATGAGCTGGAAGATCTCAACACAGCGTCCAGCAGGCGGAGGCGGCTGG 971
Db 949 AGCGAGGAATGAGCTGGAAGATCTCAACACAGCGTCCAGCAGGCGGAGGCGGCTGG 1008
QY 972 TGGCCAAACAGAGGTGATCGATAGCTGAAGGAGGAGGCGGAGCAGCAGCAAGATTGGA 1031
Db 1009 TGGCCAAACAGAGGTGATCGATAGCTGAAGGAGGAGGCGGAGCAGCAGCAAGATTGGA 1068
QY 1032 TGGAGACCGTTCCGGTGTGAAGGCGCCAGGCGGATATCTACAAGCGGACTTCCAGGCTG 1091
Db 1069 TGGAGACCGTTCCGGTGTGAAGGCGCCAGGCGGATATCTACAAGCGGACTTCCAGGCTG 1128
QY 1092 AGAGCAGCGCCGGAGAGAGCTGGCGGAGAAAGAGAGTCTCTGAGAGAGCAGCTGGAGC 1151
Db 1129 AGAGCAGCGCCGGAGAGAGCTGGCGGAGAAAGAGAGTCTCTGAGGAGCAGCTGGAGC 1188
QY 1152 AGCTGAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTGAGAGTCGGCCAGGATCGAGG 1211
Db 1189 AGCTGAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTGAGAGTCGGCCAGGATCGAGG 1248
QY 1212 ACATGAGGAAGCGCATGTGAGAGTCTCCAGGCGCCCTTGGCCCGCCCTGCTTACC 1271
Db 1249 ACATGAGGAAGCGCATGTGAGAGTCTCCAGGCGCCCTTGGCCCGCCCTGCTTACC 1308
QY 1272 TCTCTCTCCCTGCGCTGCGCAGCAGAGAGAGGCGCCCGCAGGAGCCACCTGACT 1331
Db 1309 TCTCTCTCCCTGCGCTGCGCAGCAGAGAGGAGGCGCCCGCAGGAGCCACCTGACT 1368
QY 1332 TCTGCTGTCCCAAGTGCAGTATCAGGCGCCCTGATATGACACCTGCGAGATACATGCA 1391
Db 1369 TCTGCTGTCCCAAGTGCAGTATCAGGCGCCCTGATATGACACCTGCGAGATACATGCA 1428
QY 1392 TGGAGTGCAATTGAGTAGGCGCGCCAGTGAAGGCGACTGCTGCGCCGAGGAGCAGTGGCCG 1451
Db 1429 TGGAGTGCAATTGAGTAGGCGCGCCAGTGAAGGCGACTGCTGCGCCGAGGAGCAGTGGCCG 1487
QY 1452 GGACGTCAGTCTGGGCTTTCTCTCCCGCTGCTGAGCCAGGATGAAGGGCTGGGGT 1511
Db 1488 GGACGTCAGTCTGGGCTTTCTCTCTCCCGCTGCTGAGCCAGGATGAAGGGCTGGGGT 1547
QY 1512 GCCAAGCTGGATGCCACTGGAGCCCGCAGGAGCTGCGCGGCGACCTTACGCTT 1571
Db 1548 GCCAAGCTGGATGCCACTGGAGCCCGCAGGAGCTGCGCGGCGACCTTACGCTT 1607
QY 1572 CAGCTGTTGATCCGCTGGTCCCTCTTTTGGGGTAGATGCGGCGCCCGATCAGGCTGACT 1631

Db 1608 CAGCTGTTGATCCGCTGGTCCCTCTTTTGGGGTAGATGCGGCCCGATCAGGCGCTGACT 1667
QY 1632 CGCTGCTCTTTTGTGTTCCCTTCTGCTGCTCGAACCACTTGGCTCGGGCTAATCCCTCCC 1691
Db 1668 CGCTGCTCTTTTGTGTTCCCTTCTGCTGCTCGAACCACTTGGCTCGGGCTAATCCCTCCC 1727
QY 1692 TCTTCTCTCACCCGCACTGGGGAAAGTCAAGAAATGGGGCTTGGGGCTCTCAGGGAGAACT 1751
Db 1728 TCTTCTCTCACCCGCACTGGGGAAAGTCAAGAAATGGGGCTTGGGGCTCTCAGGGAGAACT 1787
QY 1752 GCTTCCCTCGCAGAGCTGGGGTGGAGCTCTTCTCCCAACCGGACACCGGCGCCGCGC 1811
Db 1788 GCTTCCCTCGCAGAGCTGGGGTGGAGCTCTTCTCCCAACCGGACACCGGCGCCGCGCT 1847
QY 1812 GCTGTGCGCTGGAGTGTGCGCTCTTACCATGACACGGGTGCTCTCTTTTGGGCTGC 1871
Db 1848 GCTGTGCGCTGGAGTGTGCGCTCTTACCATGACACGGGTGCTCTCTTTTGGGCTGC 1907
QY 1872 ATGCTATTTCCTATTTTGCAGCCAGACCGATGTGATTTTAAACCACTCACTATTGATGACAT 1931
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RESULT 15

ADA44712
ID ADA44712 standard; DNA; 1975 BP.
XX
AC ADA44712;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 10.
XX
KW Antisense oligonucleotide; cytostatic; immunosuppressive;
KW antiinflammatory; gene therapy; hyperproliferative disorder; cancer;
KW autoimmune; inflammatory disorder; inhibitor-kappa B kinase-gamma; gene;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2003031576-A2.
XX
PD 17-APR-2003.
XX
PF 03-OCT-2002; 2002WO-US031809.
XX
PR 06-OCT-2001; 2001US-00972607.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2003-457242/43.
XX
PT New compound having sequence targeted to nucleic acid encoding inhibitor-kappa B kinase-gamma, useful for preparing composition for treating e.g., cancer, or inflammatory or autoimmune disorder.
XX
PS Example 15; Page 86-88; 106pp; English.
XX
CC The invention relates to an antisense compound that is targeted to a nucleic acid encoding inhibitor-kappa B kinase-gamma, specifically hybridising to the nucleic acid encoding inhibitor-kappa B kinase-gamma and inhibiting its expression. Compounds of the invention are antisense oligonucleotides comprising at least one modified internucleoside linkage, which is a phosphorothioate linkage, at least one modified sugar moiety, which is a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase, which is a 5-methylcytosine. Preferably, the antisense oligonucleotide is a chimeric oligonucleotide. The compound of

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 9, 2005, 02:58:23 ; Search time 240 Seconds
(without alignments)

2856.666 Million cell updates/sec

Title: US-09-377-795-2

Perfect score: 2115

Sequence: 1 MNRHLWKSQCEMVQPSGGP.....COVQAPDMDTQIHVMECIE 419

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2115	100.0	2009	4	US-09-646-403-1
2	2115	100.0	2035	4	US-09-863-049B-3
3	2028.5	95.9	2034	4	US-09-646-403-2
4	1822.5	86.2	1874	4	US-09-853-701-2
5	584.5	27.6	23106	4	US-09-863-049B-1
6	251	11.9	5883	4	US-09-949-016-5001
7	237	11.2	2812	4	US-09-702-953B-1
8	237	11.2	6644	4	US-08-875-435B-5
9	236	11.2	2934	4	US-09-010-147B-17
10	235	11.1	6175	4	US-08-875-435B-1
11	228.5	10.8	3536	4	US-09-949-016-1083
12	228.5	10.8	7218	4	US-09-949-016-1775

13	228.5	10.8	7218	4	US-09-949-016-1776	Sequence 1776, Ap
14	228.5	10.8	82125	4	US-09-949-016-13517	Sequence 13517, A
15	228.5	10.8	82125	4	US-09-949-016-13518	Sequence 13518, A
16	225	10.6	5185	4	US-09-976-594-640	Sequence 640, App
17	223.5	10.6	7596	4	US-09-023-655-1463	Sequence 1463, Ap
c 18	223	10.5	945	4	US-09-543-681A-2325	Sequence 2325, Ap
19	223	10.5	3543	4	US-09-543-681A-2264	Sequence 2264, Ap
20	222.5	10.5	6306	1	US-08-466-390-3	Sequence 3, Appli
21	222.5	10.5	6306	1	US-08-470-950-3	Sequence 3, Appli
22	222.5	10.5	6306	1	US-08-467-781-3	Sequence 3, Appli
23	222.5	10.5	6306	1	US-08-195-487-3	Sequence 3, Appli
24	222.5	10.5	6306	2	PCT-US93-06160-3	Sequence 3, Appli
25	222.5	10.5	6306	5	PCT-US93-06160-3	Sequence 3561, Ap
26	221	10.4	4806	4	US-09-949-016-3561	Sequence 296, App
27	221	10.4	4860	4	US-09-949-016-296	Sequence 248, App
28	221	10.4	7453	4	US-09-620-312D-248	Sequence 249, App
29	221	10.4	7501	4	US-09-620-312D-249	Sequence 119, App
30	221	10.4	8948	3	US-09-643-597-119	Sequence 119, App
31	221	10.4	8948	4	US-09-480-884A-119	Sequence 119, App
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34	221	10.4	8948	4	US-09-221-107-119	Sequence 119, App
35	221	10.4	8948	4	US-09-466-396A-119	Sequence 119, App
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37	221	10.4	8948	4	US-09-630-940B-119	Sequence 119, App
38	221	10.4	8948	4	US-09-285-479-119	Sequence 119, App
39	218.5	10.3	9551	1	US-08-056-200-93	Sequence 93, Appl
40	218.5	10.3	9551	2	US-08-800-644-93	Sequence 93, Appl
41	217.5	10.3	3893	4	US-09-949-016-908	Sequence 908, App
42	214.5	10.1	5574	4	US-09-917-254-40	Sequence 40, Appl
43	214.5	10.1	6861	4	US-09-949-016-1240	Sequence 1240, Ap
44	214.5	10.1	6861	4	US-09-949-016-1241	Sequence 1241, Ap
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ALIGNMENTS

RESULT 1

US-09-646-403-1
; Sequence 1, Application US/09646403
; Patent No. 6734174
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR F
; TITLE OF INVENTION: AND OTHER PROTEINS
; FILE REFERENCE: WALLACH=27
; CURRENT APPLICATION NUMBER: US/09/646,403
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: IL 123758
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: PCT/IL99/00158
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: IL 126024
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2009
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-646-403-1

Alignment Scores:
Pred. No.: 1,71e-200 Length: 2009
Score: 2115.00 Matches: 419
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-377-795-2 (1-419) x US-09-646-403-1 (1-2009)

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Qy 21 AlaAlaSerGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 214 GCAGCAGATCAGGACGTACTGGCGGAAGAGTCTCTCTGGGGAAGCCACCATGTCAC 273
Qy 41 LeuProSerGlnGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGlnGlu 60
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Qy 61 LeuArgAspAlaLeuArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80
Db 334 CTCGAGATGCCATCCGGCAGACCAACAGATTCTCGGGAGCGCTGCGAGGAGTCTTG 393
Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
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Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
Db 514 GCTCTGGGAGGTGGAGCACCCTGAAGAGATGCCAGCAGCAGATGGCTGAGACAAAGCC 573
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnLysSerArgLeu 160
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Db 754 CAGCTCGCATGTCAGGCGCAGAGCGTGGAGGCGCGCTCCGATGGAGCGCCAGCCGCC 813
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US-09-863-049B-3
; Sequence 3, Application US/09863049B
; Patent No. 6824972
; GENERAL INFORMATION:
; APPLICANT: Kenrick, Sue J.
; APPLICANT: Nelson, David L.
; APPLICANT: Aradhy, Swaroop
; APPLICANT: D'Urso, Michele
; APPLICANT: Woffendin, Hayley
; APPLICANT: Munnich, Arnold
; APPLICANT: Smahi, Asmae
; APPLICANT: Israel, Alain
; APPLICANT: Poustka, Annemarie
; APPLICANT: Lewis, Richard A
; APPLICANT: Levy, Moise
; APPLICANT: Heiss, Nina
; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Defe
; FILE REFERENCE: HO-P01961US1
; CURRENT APPLICATION NUMBER: US/09/863,049B
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/206,223
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2035
; TYPE: DNA
; ORGANISM: Human
US-09-863-049B-3
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Pred. No.: 1,75e-200 Length: 2035
Score: 2115.00 Matches: 419
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGlnGlnGlu 60
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Qy 61 LeuArgAspAlaLeuArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80
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Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
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Qy 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400
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; Sequence 2, Application US/09646403
; Patent No. 6734174
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR
; TITLE OF INVENTION: AND OTHER PROTEINS
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; FILE REFERENCE: WALLACH=27
; CURRENT APPLICATION NUMBER: US/09/646, 403
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: IL 123758
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: PCT/IL99/00158
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: IL 126024
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-646-403-2
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Query Match:	95.91%	Indels:	4
DB:	4	Gaps:	1

US-09-377-795-2 (1-419) x US-09-646-403-2 (1-2034)

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Db	232	GCAGCAGATCAGGACGTACTTGGCGGAAGAGTCTCTCTTGGGGAAGCCAGGCACTGCTGCAC	291
Qy	41	LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeu-GluGluHisGlnGln	60
Db	292	CTGCCTTCAGAACAGGGCGCTCTCTGAGACCCCTCCAGCGCTGCTGGGAGGAGAATCAAGA	351
Qy	60	uLeuArgAspAlaIleArgGln-SerAsnGlnIleLeuArgGluArgCysGlu---GluL	79
Db	352	GCTCCAGATGCCATCCGCGAGTAGCAACAGATTCTTTCGGGAGGCTGCCGAAAGGGAGCT	411
Qy	79	eLeuHis-PheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGln	98
Db	412	TTCGTGATTTTCCAGCCAGCCAGAGGAGAGAGAGTTCTCTCATGTGCAAGTTCAG	471
Qy	99	GluAlaArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLys	118
Db	472	GAGGCCAGGAAACTGTGTGGAGAGACTCGGCTTCGAGAGCTCGATCTGAAGAGGAGAGAG	531
Qy	119	GluGlnAlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAsp	138
Db	532	GAGCAGGCTCTGCGGAGGTGGAGCACCTGAAGAGATGCCAGCAGCAGAGATGGCTGAGGAC	591
Qy	139	LysAlaSerValLysAlaGlnValThrSerLeuLeuGlyLysLeuGlnGlnSerGlnSer	158
Db	592	AAGGCTCTGTGAAGACCCAGGTGAGCTCTTGTCTGGGAGCTGCAGGAGAGCCAGAGT	651
Qy	159	ArgLeuGluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAsp	178
Db	652	CGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGTCGGGCCCGGGCCGACG	711
Qy	179	GluGlnAlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGln	198
Db	712	GAGCAGCGCGGAGCTGGAGAGTGCAGCGAGCGCTGCAGCAGCAGCAGCAGCGTGCAG	771
Qy	199	ValAspGlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGln	218
Db	772	GTGGACAGCTGCGCATGAGGCGCAGAGCTGGAGCGCCGCTCGCATGGAGCGCCAG	831
Qy	219	AlaAlaSerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPhe	238

Db 832 GCCGCTCGGAGGAGAGAGAGCTGGCCCGAGCTTGCAGGTGGCCCTATCACAGAGCTCTTC 891
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Db 892 CAAGAATACGACACCATCAAGAGCAGCGTGGTGGCAGTGAGCGGAAGCGAGGAATG 951
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Db 1072 CCGGTGTCGAAGGCCCAAGGCGGATATCTACAAGCGGAGCTTCAGGCTGAGAGGCGAGGCC 1131
Qy 319 ArgGluLysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 338
Db 1132 CGGAGAGAGCTGGCCGAGAGAGGAGCTCTGCGAGGACGAGCTGAGCAGCTGAGAGG 1191
Qy 339 GluTyrSerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLys 358
Db 1192 GAGTACAGCAAACTGAAGGCCAGCTGTCAAGGCTCGGCCAGGATCGAGGACATGAGGAAG 1251
Qy 359 ArgHisValGluValSerGlnAlaProLeuProProAlaProAlaProAlaProAlaPro 378
Db 1252 CGGATGTCAGGTCTCCAGGCCCTTGGCCCGCCGCTGCTACCTCTCTCTCTCTCTCT 1311
Qy 379 LeuAlaLeuProSerGlnArgArgSerProProGluProProProAspPheCysCysPro 398
Db 1312 CTGGCCCTGCCAGCAGAGGAGGAGGCCCGCCGAGGAGCCACCTGACTTCTGCTGCTCC 1371
Qy 399 LysCysGlnTyrGlnAlaProAspMetAspThrLeuGlnHisValMetGluCysIle 418
Db 1372 AAGTGCAGTATCAGGCCCTGATATGGACACCCCTGCAGATACATGTCTATGAGTGCAAT 1431
Qy 419 Glu 419
Db 1432 GAG 1434

RESULT 4

US-09-253-701-2
; Sequence 2, Application US/09253701
; Patent No. 6680366
; GENERAL INFORMATION:
; APPLICANT: SHOJI, YAMAKA
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE ENCODING A MODULATOR OF NF-KB
; FILE REFERENCE: 0660-0146-55
; CURRENT APPLICATION NUMBER: US/09/253,701
; CURRENT FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1874
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-253-701-2

Alignment Scores:

Pred. No.:	1,91e-171	Length:	1874
Score:	1822.50	Matches:	362
Percent Similarity:	90.93%	Conservative:	19
Best Local Similarity:	86.40%	Mismatches:	31
Query Match:	86.17%	Indels:	7
DB:	4	Gaps:	1

US-09-377-795-2 (1-419) x US-09-253-701-2 (1-1874)

Qy 1 MetAsnArgHisLeuTriLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 94 ATGAACAGCACCCCTGGAGAGACCAAGCTGAGTGAGCGGTGCAGCCCGAGTGGGCCCA 153

Qy 21 AlaAlaAspGlnAspValLeuGluSerProLeuGluLysProAlaMetLeuHis 40
Db 154 GCAGAGGACCAAGGACATCTGGTGAAGAACTCTTCTGGGGAAGCCTCAATGCTACAT 213
Qy 41 LeuProSerGluGlnGlnAlaProGluThrLeuGlnArgCysLeuGluGlnGlnGlu 60
Db 214 CTGCCTTTCAGAGCAGGCTACTCTTGAAGCCCTCCAGCGCTGCTGGAAGAGAATCAAGAG 273
Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
Db 274 CTCGAGAGCGTATCCGCGACAGCAATCAGATGCTGAGGGAACGCTGTGAGAGCTGCTG 333
Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
Db 334 CATTTCCAGGTCAGCCAGCGGAGGAGAGGAGTTCCTTATGTGCAAAATTCAGGAAGCC 393
Qy 101 ArgLysLeuValGluArgLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 394 CGGAAGCTGGTGGAGAGACTGAGCTTGGAGAAGCTTGATCTTCGAGTCAGAGGAACAG 453
Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
Db 454 GCCTTAAAGAGTGGAGCAACTGNAAGAAATGCCAAGCAGAGATGCTGAGGACAGGCGC 513
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGluGlnGlnGlnSerGlnSerArgLeu 160
Db 514 TCTGTGAAGCTCAGGTGACATCTTGTCTCGAGAACTCCAGGAGAGCCAGAGCGGTTTG 573
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 574 GAGCTGCCCAAGGATCGCAAGCTTTAGAGGAAGGATTCGAGCGAGTTAGTCAGCAG 633
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
Db 634 GTCAGACAGCTGGAGAGTGAGCGGAGGTGCTACAGCAGCAGCAGCAGGCTCCAGGTGAC 693
Qy 201 GlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 694 CAGCTGCTATGCAAGAACCAAGCGTGGAGGCTGCTCTTGGAAATGGAGCGGAGCTGCT 753
Qy 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
Db 754 TCAGAGGAGAAAGCGAGCTGGCTCAGTTCGAGCAGCAGCTATCACCAGCTCTTCCAGAC 813
Qy 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 814 TAGCACAGCCACATTAAGAGCAGC-----AAGGGCATGCAGCTG 852
Qy 261 GluAspLysLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 853 GAAGATCTGAGGCACACAGCTCCAGCAAGCTGAGAGGCGCCCTGGTAGCCAAACAGGAATG 912
Qy 281 IleAspLysLeuLysGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db 913 ATTGATAAGCTGAAGAGGAGGCTGAGCAGCAGCAAGATTGTGTGAGGAGCTGTGCCAGTC 972
Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 973 TTGAAGGCCCGAGCGGATATCTCAAGGCTGACTTCAAGCTGAGAGGCGCATGCCCGGAG 1032
Qy 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnGlnArgGluTyr 340
Db 1033 AAGCTGGTGAGAGAAAGAGGATATTTCAGAGCAGCAGCTGAGCAGCTGAGCGGAGTTC 1092
Qy 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
Db 1093 AACAAAGCTGAAGTGGCTGCCATGAGTCAGCAGGATTGAGGATATGAGGAAGCGCAT 1152
Qy 361 ValGluValSerGlnAlaProLeuProProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 1153 GTAGAGACTCCCGAGCGCTCTTTACTCCCTGCTCCAGCTCACCAGCTCCTTTTCATTGTC 1212

QY 256 ----- 256
Db 19581 GAACCTTGAGANTGGGTCCTGCCTTAGACTTGTGCTTAGACCTGTGTACAGCTGCAGCTGC 19640
QY 256 ----- 256
Db 19641 GACAGCTCAGGAAGCTGTGGGGAGATGGCAACCCAGGATGTGTCTCAGGAGTGCA 19700
QY 256 ----- 256
Db 19701 GCAGGCCATCTTAATGGGGGGCTGGGCCAGAGCCTTGGGGTGTCTCCCTCTGTGGGGCTGG 19760
QY 256 ----- 256
Db 19761 GGAGCTCTTGTCTCCATGGACATTCCTCTTGCAGCCATCGCCATCTGGACCTGGGCTC 19820
QY 256 ----- 256
Db 19821 AGCTTCCCCCAAGCAAGGTAAGCCGACAGCATTTCCACCCAGTGTGTGGCTGGGAGCC 19880
QY 256 ----- 256
Db 19881 TTTTCTAGTTGTCTCATCAGACCTAAGCTGGGTGCAGTTTGTCTAGTGTATCACAATTT 19940
QY 256 ----- 256
Db 19941 TAGCAGGACACCTCAATCGTAAGTGTACCCAGAGGAGATTTATAAGGACAAGCCTGAA 20000
QY 256 ----- 256
Db 20001 GCCAGGTACATGGGAAGATGTAGCTACAAAACCTGGCCACTTAATCTCTGGAGGGGGC 20060
QY 256 ----- 256
Db 20061 GTTGGTGGGTGTGTGTGTGTCTCAGGGGGCTGGAGATGCTCGGTGGAGGAGTG 20120
QY 256 ----- 256
Db 20121 CACCTCTGACAGGTGGCAGAGTGAAGGACTGAGGGCTCTCAGCTGAGCTGTGCACATG 20180
QY 256 ----- 256
Db 20181 GCGGGCACAGGACCGGCTGGCTGTGAGTGGGTGTGGCCTGTGGCCTGTGAAGGTGGGAG 20240
QY 256 ----- 256
Db 20241 GAGGGCTGTGAGCTGGGATTTCTGGGAAGGGAATGTGGGCCAGCTGGGAGGTTGTACC 20300
QY 256 ----- 256
Db 20301 AGATGACCTCAGCGGCTCTTCAGTCTCTGAAAAAACCTCAGCATCTCCTCTGTCTGTTT 20360
QY 256 ----- 256
Db 20361 GGGCCGTGACAGACAGCCATCTCCCTGTGACGCTGAGATCTGCAATGGGCCCTCA 20420
QY 256 ----- 256
Db 20421 AATCAGGGCTGGCATCACCAGCTGTGTCAGCCAGGGCCACTCTTTTCATCCTTCTCAGT 20480
QY 256 ----- 256
Db 20481 TCTTCTCAGCAGCCTCGCCCTGGGCTGACAGGCTCGCTCAGCTCCCTTTGCCCGTCT 20540
QY 257 ---GlyMetGlnLeuAspLeuLysGlnLeuGlnAlaGluGluAlaLeuVal 275
Db 20541 TAGGGATCGACTGAAGATCTCAACAGACAGCTCCAGCAGGCGGAGGAGGCTGGTG 20600
QY 276 AlaLysGlnValIleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMet 295
Db 20601 GCCAAACAGAGGTGATCGATAAGCTGAAGGAGGAGCGCGAGCAGACAAATGTGTATG 20660
QY 296 GluThrValProValLeuLysAla----- 303

Db 20661 |||||GAGACCGTTCCGGTCTGAAGGCCCGAGGTGAGGGCCCTCTCTCTGACCCACCTGGCAC 20720
QY 303 ----- 303
Db 20721 TGGGACCTGGAGAGTCTCTTTGGCGTCTTTTGTGCTTTTGTCTTTGCTTTGCTTTGAGA 20780
QY 303 ----- 303
Db 20781 TTGAGTTTGTCTTTGTTGCCAGGCTGGAGTGCCACTAGTGGCACGATCTTGGCTCACT 20840
QY 303 ----- 303
Db 20841 GCAACCTCTGCCTTCGGGGTTCAACAATCTCTTTTGGCTCAGCCTCTCTGAGTAGCTGG 20900
QY 303 ----- 303
Db 20901 ATTACAGCGCCTGCGCCATGCCCGTCTAATTTTGTATTTTATAGTAGACAGAGGTTT 20960
QY 303 ----- 303
Db 20961 CACCATGTTGGCCAGCTGTCTCGAACTTCTGGCCTCAGGTGATCTGCCACCGCAGTC 21020
QY 303 ----- 303
Db 21021 TCTCAAGTCTGGATTACAGGCGTGAGCCACCGCCCTCTTTGGCATCATTTT 21080
QY 303 ----- 303
Db 21081 GTAGTGGCTTTCGTAACTTCTGAGCCACTTGTGTCTCTCTTAGACCTCTCGGTGAGC 21140
QY 303 ----- 303
Db 21141 TTGCAATTACTGCGCAGTATCTGTTTCTCTGACCGCTGGGGCTCTGGGAGGACAG 21200
QY 303 ----- 303
Db 21201 CAGTGGGTCTGTCTTGTCTGTGCTGCGCAGTCTGTGGTGGTGGCTGGCTG 21260
QY 304 -----GlnAlaAspIleTyrLysAlaAspPheG1 313
Db 21261 TGGCGGCGACATCCCTTTCTGTGGATTGTGCGCGGATATCTACAAGCGGACTTCCA 21320
QY 313 nAlaGluArgGlnAlaArgGluLysLeuAlaGluLysGlnLeuGlnGlnLe 333
Db 21321 GCCTGAGGAGGAGCGCGGAGAGCTGGCGGAGAGGAGCTCTGAGAGGAGCAGCT 21380
QY 333 uGluGlnLeuGlnArgGluTyrSerLysLeuLysAlaSerCysGlnGluSerAla- 351
Db 21381 GGAGCAGCTGCAGAGGAGTACAGCAAACTGAAGGCCAGCTGTCAAGGAGTCGGC-CAGGT 21439
QY 351 ----- 351
Db 21440 GGGCTCTGAGAGCGTCCCGTGTGAGCAGTGGGTGGGACACTGGGGGTGCCAGTGTG 21499
QY 351 ----- 351
Db 21500 GACCCCGAGTGGTGCACACACTGGGGGGTGGCCAGTGTGTGACCAAGGAGCAGGATGGC 21559
QY 351 ----- 351
Db 21560 TCCTGTGTCTGTGGTTAGGGCTCAGTGTGTCTCTCTCTCTCAGCTTCCAAGA 21619
QY 351 ----- 351
Db 21620 GCTGCTTTGACATGATCCAGCAAGAGGCTTTACAGAAATGCGTGGCTTCACTGGACGG 21679
QY 352 -----ArgIleGluAspMetArgLysArgHisValGluValSerGlnAlaPr 367
Db 21680 TTTCTGTTTCAAAAGATCGAGGACATGAGGAGCGGCAATGTGAGGGTCTCCAGGCCCC 21739
QY 367 oLeuProProAla----- 371
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Db 21740 CTTGCCCCGCCCTCGTGTGAGTGAGCGAGAACTGGGCTCGGGAGGAGGTGGTGGG 21799
QY 371 ----- 371
Db 21800 AGGCAGGTGTCGGCCGCGGAGGTACAGTTGCGACTTCTCTGTTGCTCTCTGGAGACT 21859
QY 371 ----- 371
Db 21860 TGACGGCGGAGTCTGTGTAGGCCACCCATCGGTAGCCACCCCTTCCCGGAGGCTAA 21919
QY 371 ----- 371
Db 21920 GGGAGGCATCGGTGTAGCGGCGCTCTGTCTTATCATGAGTGGCTGTGAGACCAGG 21979
QY 371 ----- 371
Db 21980 CTTGCCATTGACAGTCTCGCCAGTCTCCGTCCCTCCCTCCCTCCCTCTCTGACT 22039
QY 372 -----ProAlaTyLeuSerSerProLeuAlaLeuProSerGlnArgSerP 388
Db 22040 CTTCTCTTTTCCAGCCTACTCTCTCTCTCCCTGCGCTGCGCCAGCCAGAGGAGGCC 22099
QY 388 roProGluGluProProAspPheCysCysProLysCysGlnTyrglnAlaProAspMetA 408
Db 22100 CCCCCGAGGAGCCACCTGACTTCTGTCTGTCCCAAGTGCACATATCAGGCCCTGATATGG 22159
QY 408 spThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 22160 ACACCTTGCAGATACATGTATGAGTGCAATTGAG 22194

RESULT 6

US-09-949-016-5001
; Sequence 5001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5001
; LENGTH: 5883
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5001

Alignment Scores:
Pred. No.: 2,1e-14 Length: 5883
Score: 251.00 Matches: 111
Percent Similarity: 39.79% Conservative: 80
Best Local Similarity: 23.12% Mismatches: 132
Query Match: 11.87% Indels: 157
DB: 4 Gaps: 20

US-09-377-795-2 (1-419) x US-09-949-016-5001 (1-5883)

QY 6 TrpLysSerGlnLeu-----CysGluMetValGlnProSerGlyProAlaA 22
Db 2268 TGGCCAGAGCAAGTCTTCTTCGCTGCGGTGTGCTGGCCACCTCGAGGAGGAGCGAGA 2327
QY 23 AspGlnAsp-----ValLeuGluGlu 29
Db 2328 CCTGAAGATCACCGACGTATCATAGGTTCCAGGCTGTGTGAGGGGCTTACCTGGCCAG 2387

QY 30 GluSerProLeuGlyLysProAlaMetLeuHisLeuProSerGluGlnGlyAlaProGlu 49
Db 2388 GAAAGCATTTGCCAAGCGGAGCAGAGCTTAC-----CGCCATGAGGTCTCTCCAGCG 2441
QY 50 ThrLeuGlnArgCysLeuGluGluAenGlnGluLeuArg-----AspAlaIleArgGln 67
Db 2442 GAACTG---CGCTGCTTACCTGAAGCTGCGGAACTGCGAGTGGTGGCGGCTCTTCCACAA 2498
QY 68 Ser-AsnGlnIleLeuArgGluArgCysGluGluLeuHisPheGlnAlaSerGlnAr 87
Db 2499 GGTCAAGCCCTGCTG-----CAGGTGAGCCCGGCA 2528
QY 87 gGluGluLysGluPheLeuMetCysLysPheGlnGluAlaAargLysLeuValGluA 107
Db 2529 GGAGGAGGAG-----ATGATGCCAAGGAGGAGGAGCTGGTGAAGTTCAGAGAAG-- 2580
QY 107 uGlyLeuGluLysLeuAspLysArgGlnLysGluGlnAlaLeuArgGluValGluHI 127
Db 2581 -----CAGCTGGCTGCGGAGAACAGGCTCACCGAGATGGAGAC 2618
QY 127 steLysArgCysGlnGlnMetAlaGluAspLysAlaSerValLysAlaGlnVal-- 146
Db 2619 GCTG-----CAGTCTCAGCTCATGCGCAGAGAAATTCAGCTGCAGAGCAGCTCCA 2669
QY 147 -----ThrSerLeuLeuGlyGluGlnSerGlnSerArgLeuGluAlaA 164
Db 2670 GGCAGAAACCGAGCTGTGTGCGGAGCTGAGGAGCTCCGGCGCCCTGACCCGCAAGAA 2729
QY 164 rLysGlu-----CysGlnAlaLeuGlyArgAlaAargAlaA 180
Db 2730 GCAGGAATTAGAAAGAGATCTGCATCAGCTAGAGCCAGGCTGGAGGAGGAGGAGCG 2789
QY 180 nAlaArgGlnLeuLysSerGluArgGluAlaLeuGlnGlnHisSerValGlnValAs 200
Db 2790 CTGCCAGCACCTGCAGCGGAGAAAGAGATGCAGCAGAAATCCAGAGCTTGAGGA 2849
QY 200 pGlnLeuArgMetGlnGlnSerValGluAlaA 217
Db 2850 GCAGCTGGAG---GAGGAGGAGAGCCCGCGCAGAGAGCTGCAGCTGGAGAGGTGACCAC 2906
QY 218 -----G1 218
Db 2907 CGAGGCGAAGCTGAAAAAGCTGGAGGAGGAGCAGATCATCTCTGGAGGACCAGAACTCAA 2966
QY 218 nAlaAlaSerGluGluLys----- 224
Db 2967 GCTGCGCCAGGAAAGAAAAGAACTGCTGGAAGACAGAAATAGTGTGAGTTCACCAACCTCAC 3026
QY 225 -----ArgLysLeuAlaGlnLeuGlnValAlaTyHisGlnLeuPh 238
Db 3027 AGNAGAGGAGGAGAAATCTTAAGAGCTCCCAAGCTCAAGAACAGCATGAGGCAATGAT 3086
QY 238 eGlnGluTyArgAsnHisIleLysSerValValGlySerGluArgLysArgGlyMe 258
Db 3087 CACTGACTTGGAAAGAGCGCTCCGC-----AGGAGGAGAGAGCAGCGACA 3131
QY 258 tGlnLeuGlu----- 261
Db 3132 GGAGCTGGAGAGAGACCCCGCGGAGGAGGAGACTCCACAGACCTTCAGCGACCCAGAT 3191
QY 262 -----AspLeuLysGlnGlnGlnAlaGluGluAl 273
Db 3192 CGCCGAGCTCCAGGCCACAGATCGCGAGGCTCAAGATGTCAGCTGGCCAAAGAGGAGGA 3251
QY 273 aLeuValAlaLysGlnGluValIleAspLysLeuLysGluGluAlaGluGlnHisI 293
Db 3252 GCTC-----CAGGCCCGCTCGCAGAGTGGAGAGAGAGCTGCCCAGAGAAGACAT 3302
QY 293 eValMetGluThrValProValLeuLysAlaGlnAlaAspIleTyLysAlaAspPheG 313
Db 3303 GGCCTTCAAGAGATCCGGGAGCTGGAATCTCAGATCTCTGAACCTCCAGGAGACCTGGA 3362
QY 313 nAlaGluArgGlnAlaArgGluLysLeuAlaGluLysLysGluLeuGlnGlnLe 333


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Qy 371 -----AlaProLysLeuSerProLeuAlaLeuProSerGlnArgArgse 387
Db 1812 CCACCCATGCCAGCCATGGTACCTCACCATGGCTTACAAGGACTGG-TCCCAGATCCGATA 1870
Qy 387 rProPro-----GluGluProProAsp-----PheCy 396
Db 1871 CCCTCCACCCCTGTGCCCCATGGAGCACCGCGCCCCACACCCCAACTCTCGCCTCTTTCCA 1930
Qy 396 sCyProLysCysGlnTyrGlnAlaPro 405
Db 1931 TCTGCCGGAGTACACCTGGCGTCCACCC 1958

RESULT 8
US-08-875-435B-5
; Sequence 5, Application US/08875435B
; Patent No. 6593304
; GENERAL INFORMATION:
; APPLICANT: Hasegawa, Kazuhide
; APPLICANT: Arakawa, Emi
; APPLICANT: Oda, Shoji
; APPLICANT: Matsuda, Yuzuru
; APPLICANT: Takahashi, Katsuhito
; APPLICANT: Sugahara, Michihito
; APPLICANT: Ishiyama, Haruo
; TITLE OF INVENTION: RECOMBINANT DNA COMPRISING DNA CODING
; TITLE OF INVENTION: FOR MYOSIN HEAVY CHAIN SM1 ISOFORM PROTEIN INSERTED INTO
; TITLE OF INVENTION: VECTOR DNA, MICROORGANISM CARRYING THE RECOMBINANT DNA, AND
; TITLE OF INVENTION: AN AGENT FOR TREATMENT OF ARTERIOSCLEROSIS COMPRISING THE
; TITLE OF INVENTION: RECOMBINANT DNA
; FILE REFERENCE: 07898-013001
; CURRENT APPLICATION NUMBER: US/08/875,435B
; CURRENT FILING DATE: 1997-07-25
; PRIOR APPLICATION NUMBER: PCT/JP96/00134
; PRIOR FILING DATE: 1996-01-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6644
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-08-875-435B-5

Alignment Scores:
Pred. No.: 6,19e-13 Length: 6644
Score: 237.00 Matches: 114
Percent Similarity: 40.20% Conservative: 83
Best Local Similarity: 23.27% Mismatches: 138
Query Match: 11.21% Indels: 155
DB: 4 Gaps: 21

US-09-377-795-2 (1-419) x US-08-875-435B-5 (1-6644)

Qy 4 HisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGly---GlyPro----- 20
Db 2316 CATGATGGGAAGCAAGCCCTGTCATCTTCTCATGATCAAAAGCTCTGGAACCTGGACCCCAACTT 2375
Qy 21 -----AlaAlaAspGlnAspValLeu-----GlyGluGluSerProLeuGlyLys 35
Db 2376 GTACAGATCGGGCAGAGCAAAATCTTCTTCCGACCGGGCGTCTGGCCCACTTGGAGGA 2435
Qy 36 ProAlaMetLeuHis-----Leu 41
Db 2436 GGAGCGGACTTGAAGATCACCGACTCATGTCATGGCTTCCAGGCCATGTGTGCTGCTA 2495
Qy 42 ProSerGluGlnGlyAla-----Pro 48
Db 2496 CCTCGCCCGCAAGGCTTCCCAAGCGGCGAGCAGCAGCTGACCGCCATGAAGTGTATCCA 2555
Qy 49 GluThrLeuGlnArgCysLeuGluGluAsnGlnGluLeuArgAspAlaIle-ArgGlnSe 68
Db 2556 GAGGAAGTGGCGGC---CTACTGAAGCTGCGGAAGCTGCA---GTGGTGGCGC----- 2604
Qy 68 rAsnGlnIleLeuArgGluArgCysGluGluLeuHisPheGlnAlaSerGlnArgG1 88

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Db 2605 -----CTTCTCACCAGGTGAAGCCGCTGCTG-----CAGGTGACACGGCAGGA 2648
Qy 88 uGluLysGluPheLeuMetCysLysPheGlnGluAlaArgLysLeuValGluArgLeuG1 108
Db 2649 GGAGGAG-----ATGCAGGCCAAGAGGATGAGCTGCAGAAAGATCAAGAGCGA----- 2697
Qy 108 yLeuGluLysLeuAspLeuLysArgGlnLysGluGlnAlaLeuArgGluValGluHisLe 128
Db 2698 -----CAGCAAGAGCGCGAGAGCGAGCTCCAGGAGCT 2729
Qy 128 uLysArgCysGlnGlnMetAlaGluAspLysAlaSerValLysAlaGlnVal----- 146
Db 2730 GCAGCAGAAGCACACGAGCTGCCGAGGAGAAAGAACTCTGTCAGGAGCAGCTGCAGGC 2789
Qy 147 ----ThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeuGluAlaThrLy 165
Db 2790 GGAGACGGAGCTGTACCGGAGGCCGAGGAGATGCGCGTCCGCTGGCGGCCAAGAAAGCA 2849
Qy 165 sGluCysGln-----AlaLeuGluGlyArgAlaArgAlaAlaSerGluGlnAl 181
Db 2850 GGAGCTGGAGGAAATCTGTCATGAGATGGAGGCCCGCTGGAGGAGGAGGAGAACCGGGG 2909
Qy 181 aArgGlnLeuLeuSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAspG1 201
Db 2910 CCAGCAGCTGCAGGCCGAGAGGAAAGATGGCCCGCAGCAGATGCTGGACCTGGAAGAGCA 2969
Qy 201 nLeu-----ArgMetGlnGlyGlnSerValGluAlaLe 213
Db 2970 ACTGGAGGAGGAGGAAAGCTGCCAGGCAGAAAGCTACAGCTCGAAAAGGTCTACCGCCGAGGC 3029
Qy 213 uArgMetGluArg----- 217
Db 3030 CAAGATCAAGAAGTTGGAGACGACATCTCTGTCATGGACGATCAGAACACAAAGCTCTC 3089
Qy 218 -----GlnAlaAlaSe 221
Db 3090 AAAAGAGCGAAACTCTTGAAGAGAGGATTAGTGATTTTAAACAATAATCTTCCGAGGA 3149
Qy 221 rGluGluLysArgLys---LeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnG1 240
Db 3150 GGAAGAGAAGGCCAAGAACCTTGACCAAGCTGGAAGAACAAGATGAATCCATGATCTCAGA 3209
Qy 240 uTyrAspAsnHisIleLysSerSerValValGlySerGluArg-----LysAr 256
Db 3210 ACTGGAAGTGGCGCTGAAGAGGAGAGAGAGCCGCGCAGAGCTGGAGAAGCTGAAGCG 3269
Qy 256 gGlyMet-----GlnLe 260
Db 3270 GAAGATGGACGGCGAGGCCAGTGACCTCCACGAGCAGATCGCCGACCTCCAGGCGCAGAT 3329
Qy 260 uGluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVa 280
Db 3330 CGCAGAGCTCAAGATGATCAGCTGGCCCAAGAGGAGAGGAGCTG-----CAGGCGGC 3380
Qy 280 lIleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVa 300
Db 3381 CTGGCCAGCTGGAGATGAACGTCTCAGAAGAACAACGCCCTCGAAGAAGATCCGGGA 3440
Qy 300 lLeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgG1 320
Db 3441 GCTGGAGGGGCACATCTCCGACCTGCAGAGGAGCCTGGACTCAGAGGGGGCCGCCAGGAA 3500
Qy 320 uLysLeuAlaGluLysGluLeuGlnGlnGlnGlnLeuGlnGlnLeu----- 336
Db 3501 CAAGGCCGAGAAGCAGACGAGACCTGGGGGAGGAGCTGGAGGCGCTGAAGACGGAGCT 3560
Qy 337 -----GlnArgG1 339
Db 3561 GGAGGACAGCTGGACACCGGCCACCCAGCAGGAGCTCCGGGGCCAAAGCGGGAGCAGGA 3620
Qy 339 uTyrSerLysLeuLysAlaSerCysGlnGlu-----SerAlaArgIleG1 354

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Pred. No.:	1.77e-10	Length:	82125
Score:	228.50	Matches:	112

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: February 9, 2005, 03:17:44 ; Search time 1630 Seconds
(without alignments)
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Title: US-09-377-795-2
Perfect score: 2115
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0
Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
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Database : Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2115	100.0	1994	10	US-09-972-607-3 Sequence 3, Appli
2	2115	100.0	1994	10	US-09-851-673-1 Sequence 1, Appli
3	2115	100.0	1994	17	US-10-628-841-3 Sequence 3, Appli
4	2115	100.0	2009	18	US-10-761-370-1 Sequence 1, Appli
5	2115	100.0	2035	10	US-09-863-049A-3 Sequence 3, Appli
6	2105	99.5	1975	10	US-09-972-607-10 Sequence 10, Appl
7	2105	99.5	1975	17	US-10-628-841-10 Sequence 2, Appli
8	2028.5	95.9	2034	18	US-10-761-370-2 Sequence 4, Appli
9	1840.5	87.0	1104	18	US-10-792-063-4 Sequence 2, Appli
10	1822.5	86.2	1874	14	US-10-189-388-2 Sequence 8, Appli
11	1822.5	86.2	1874	17	US-10-408-305-2 Sequence 2, Appli
12	827	39.1	486	18	US-10-792-063-8 Sequence 8, Appli
13	756.5	35.8	483	18	US-10-792-063-6 Sequence 6, Appli
14	584.5	27.6	23106	10	US-09-863-049A-1 Sequence 1, Appli
C 15	443	20.9	2803	9	US-09-925-298-84 Sequence 84, Appl
C 16	443	20.9	2803	14	US-10-102-806-84 Sequence 11, Appl
17	436.5	20.6	1925	18	US-10-609-133-11 Sequence 13, Appl
18	436.5	20.6	2076	18	US-10-609-133-13 Sequence 9, Appli
19	430.5	20.4	2023	18	US-10-609-133-9 Sequence 1, Appli
20	420.5	19.9	1734	17	US-10-627-757-1 Sequence 3, Appli
21	420.5	19.9	1856	18	US-10-609-133-3 Sequence 5, Appli
22	420.5	19.9	2008	18	US-10-609-133-5 Sequence 1, Appli
23	420.5	19.9	2077	18	US-10-609-133-1 Sequence 128, App
24	420.5	19.9	2139	17	US-10-172-118-128 Sequence 128, App
25	420.5	19.9	2139	17	US-10-342-887-128 Sequence 79, Appl
26	420.5	19.9	2139	18	US-10-717-597-79 Sequence 213, App
27	420.5	19.9	2327	18	US-10-755-889-213 Sequence 17, Appl
28	416	19.7	1799	18	US-10-609-133-17 Sequence 69, Appl
29	414	19.6	1908	17	US-10-136-728-69 Sequence 71, Appl
30	411.5	19.4	1908	17	US-10-136-728-71 Sequence 15, Appl
31	410	19.4	1787	18	US-10-609-133-15 Sequence 12702, A
32	359	17.0	597	16	US-10-029-386-12702 Sequence 2339, Ap
33	357	16.9	236	10	US-09-918-995-2339 Sequence 26402, A
34	349	16.5	216	16	US-10-029-386-26402 Sequence 9902, Ap
35	334	15.8	526	16	US-10-029-386-9902 Sequence 23602, A
36	332	15.7	197	16	US-10-029-386-23602 Sequence 10, Appl
37	332	15.7	264	18	US-10-792-063-10 Sequence 1505, Ap
38	252	11.9	6354	15	US-09-917-800A-1505 Sequence 1780, Ap
39	251.5	11.9	15231	9	US-10-152-319A-1780 Sequence 35, Appl
40	251.5	11.9	15231	17	US-10-028-248A-35 Sequence 35, Appl
41	249	11.8	7396	17	US-10-107-782-35 Sequence 1601, Ap
42	249	11.8	7396	17	US-09-954-456-1601 Sequence 61, Appl
43	248.5	11.7	14800	9	US-10-269-909-61 Sequence 183, App
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ALIGNMENTS

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; Sequence 3, Application US/09972607
; Publication No. US20030105037A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: JACQUELINE WYATT
; FILE REFERENCE: RTS-0191
; CURRENT APPLICATION NUMBER: US/09/972,607
; CURRENT FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (149) ... (1408)
US-09-972-607-3

Alignment Scores:

Pred. No.: 1.59e-172 Length: 1994
Score: 2115.00 Matches: 419
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-377-795-2 (1-419) x US-09-972-607-3 (1-1994)

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QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60
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QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
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QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
DB 449 AGGAACTGTGTGAGAGACTCGGCTTGGAGAGCTCGATCTGAAGAGGCGAAGAGGAGG 508
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
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QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnSerGlnSerArgLeu 160
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QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyValArgAlaArgAlaAlaSerGluGln 180
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QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
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QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
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DB 1289 CTGCCAGCAGAGGAGGAGCCCCCCCCGAGGAGCCACTGACTTCTGCTGTCTCCAGTGC 1348
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
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; Sequence 1, Application US/09851673
; Publication No. US20030165985A1
; GENERAL INFORMATION:
; APPLICANT: Derry, Jonathan
; APPLICANT: Fanslow, William
; APPLICANT: Dougall, William
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
; FILE REFERENCE: 3198
; CURRENT APPLICATION NUMBER: US/09/851.673
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (149)..(1405)
US-09-851-673-1

Alignment Scores:
Pred. No.: 1.59e-172 Length: 1994
Score: 2115.00 Matches: 419
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-377-795-2 (1-419) x US-09-851-673-1 (1-1994)

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QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60
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Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerArgLeu 160
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Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 629 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGTCGGGCCCGGGCGGCGAGGAGCAG 688
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGlnValAsp 200
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Db 869 TACGACAAACACATCAAGAGCAGCGTGTGGCGAGTGCAGCGAGCCAGGAAATGCACGTG 928
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Db 989 ATCGATAGCTTGAAGGAGGAGGCGCAGCAGCAGCAAGATTGTGATGGAGACCGTTTCCGGTG 1048
Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
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Qy 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnLeuGlnLeuGlnArgGluTyr 340
Db 1109 AAGCTGGCCGAGAAAGAGGAGCTCTGCAGAGCAGCTGGAGCAGCTGCAGAGGAGTAC 1168
Qy 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
Db 1169 AGCAACTGAAGGCCAGCTGTCAAGAGTGGCGCAGGATCAGGACATCAGAGAGCGGCAT 1228
Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 1229 GTCGAGGTCTCCAGGCCCCCTTGGCCCCCGCCCTGCTACCTCTCTCTCCCTTGCC 1288
Qy 381 LeuProSerGlnArgArgSerProProGluProProAspPheCysCysProLysCys 400
Db 1289 CTGCCCCAGCAGAGGAGGAGCCCCCGGAGGAGCCACTGACTTCTGCTGCCCAAGTGC 1348
Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
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RESULT 3

US-10-628-841-3

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; Sequence 3, Application US/10628841
; Publication No. US20040023918A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
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; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION
; FILE REFERENCE: RTS-0191
; CURRENT APPLICATION NUMBER: US/10/628,841
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/972,607
; PRIOR FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (149)...(1408)
; US-10-628-841-3
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Alignment Scores:

Pred. No.:	1,59e-172	Length:	1994
Score:	2115.00	Matches:	419
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-09-377-795-2 (1-419) x US-10-628-841-3 (1-1994)

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Qy 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 209 GCAGCAGATCAGGACGCTACTGGGCGAAGAGTCTCTCTCTGGGGAAGCAGCCATGCTGCAC 268
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
Db 269 CTGCCTTCAGAAACAGGCGCTCTCTGAGACCTCTCAGCCCTGCTGGAGGAGAAATCAAGAG 328
Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80
Db 329 CTCGAGATGTCATCCGGCAGAGCAACCAAGATTCTCGGAGGCGCTGCGAGGAGCTTCTG 388
Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
Db 389 CATTTCCAGCCAGCCAGAGGAGGAGAGGAGTCTCTCATGTGCAAGTTCAGAGAGGCC 448
Qy 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 449 AGGAAACTGGTGGAGAGACTCGGCTCGGAGAGCTCGATCTGAAGAGCAGAGGAGGAGCAG 508
Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
Db 509 GCTCTCGGAGAGTGGAGCACCTCGAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 568
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
Db 569 TCTGTGAAGCCAGGTGAGCTCTTCTCGGGAGCTGCAGGAGCAGCAGTGCAGTCTG 628
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 629 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGTCGGGCCCGGGCGGCGAGGAGCAG 688
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
Db 689 GCGCGCAGCTGGAGAGTGGCGGAGGCGCTGCAGCAGCAGCAGCAGCAGCTGCGAGGTGGAC 748
Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 749 CAGCTGGCATGCGAGGCCAGAGCGTGGAGGCGCGCTCCGATGGAGCGCCAGGCGGCC 808
Qy 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
Db 809 TCGGAGGAGAAAGAAAGTGGCCAGTTGCGAGTGGCCCTATCACAGCTCTTCCAAAGAA 868
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QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 869 TACGACCAACCAATCAAGAGAGCGTGTGGCGAGTGCAGCGAAGCAGGATGCAGCTG 928
QY 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGlnVal 280
Db 929 GAGATCTCAACAGCAGCTCCACAGCGCCAGAGGCCCTGTGTGCCAAACAGGAGGTG 988
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db 989 ATCGATAAGCTGAAGGAGGAGCGCAGCAGCACAAGATTGTGATGAGACCGTTCGCGTG 1048
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 1049 CTGAGGCCCAAGCGGATATCTACAGCGGACTTCCAGGCTGAGAGGCGGCCGCGGAG 1108
QY 321 LysLeuAlaGluLysGluLeuLeuGlnGlnLeuGlnGlnLeuGlnArgGluTyr 340
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Db 1169 AGCAAACTGAAGCGCAGCTGTGAGGAGTCGCCCAGGATCGAGGACATGAGGAAGCGCAT 1228
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLysSerSerProLeuAla 380
Db 1229 GTCAGGTCTCCAGGCCCTTGCCTCCCGCCCTGCTACCTCTCTCTCTCTCTCTCTCTCT 1288
QY 381 LeuProSerGlnArgArgSerProGluGluProGluGluProGluGluProGluGluCys 400
Db 1289 CTGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1348
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 1349 CAGTATCAGGCCCTGATATGAGCACCCTGCAGATACATGTATGAGTGCATTGAG 1405

RESULT 4

US-10-761-370-1
; Sequence 1, Application US/10761370
; Publication No. US20040219615A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR F
; TITLE OF INVENTION: AND OTHER PROTEINS
; FILE REFERENCE: WALLACH-27
; CURRENT APPLICATION NUMBER: US/10/761,370
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: US/09/646,403
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: IL 123758
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: PCT/IL99/00158
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: IL 126024
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 2009
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-761-370-1

Alignment Scores:
Pred. No.: 1,61e-172 Length: 2009
Score: 2115.00 Matches: 419
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-377-795-2 (1-419) x US-10-761-370-1 (1-2009)

QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 154 ATGATATAGCACCTCTGGAAGAGCCACTGTGTGAGATGGTGCAGCCCATGTGTGCCCCG 213
QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 214 GCAGCAGATCAGGACGTACTGGCGGAAGAGTCTCTCTCTGGGGAAGCCACCCATGTCTGCAC 273
QY 41 LeuProSerGluGlnGlnValAlaProGluThrLeuGlnArgCysLeuGluGlnGlnGlu 60
Db 274 CTGCTCTTCAAGAACAGGCGCTCTGAGACCCCTCCAGCGCTGCTGAGGAGGAATCAAGAG 333
QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
Db 334 CTCGAGATGTCATCCGCGCAGACACACAGATTCTGCGGAGCGCTGCGAGAGGCTTCTG 393
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
Db 394 CATTTCCAAGCCAGCCAGAGGAGGAGAGGAGTTCCTCATGTGCAAGTTCCAGGAGGCC 453
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 454 AGGAACCTGGTGGAGAGACTCGGCTTGGAGAGGCTCGATCTCAAGAGGAGGAGGAGCAG 513
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
Db 514 GCTCTCGGAGAGTGGAGCACCCTGAGAGATGCCAGCAGCAGATGGCTGAGGACAGGCC 573
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
Db 574 TCTGTGAAGCCAGCTGACGTCTTCTGTCGGGAGCTGCGAGGAGGAGCAGAGTCCGCTG 633
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGluValArgAlaArgAlaSerGluGln 180
Db 634 GAGGCTGCCACTAAGGAATGCCAGCTCTGGAGGGTTCGGGCCCGGCGCCGAGGAGCAG 693
QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
Db 694 GCGCGCAGCTGGAGAGTGGAGCGCGCTGCGAGCAGCAGCAGCAGCAGCTGCAGGTGCAG 753
QY 201 GlnLeuArgMetGlnGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 754 CAGTGGCGATGACAGGCGCAGAGCTGGAGCGCGCTCCGCTCCGATGGAGCGCAGGCCCC 813
QY 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
Db 814 TCGGAGGAGAGAGGAGAGTGGCCACTTGCAGGTGGCTATCACCAGCTCTTCCAGAA 873
QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 874 TACGACAAACCAATCAAGAGCAGCGTGTGGCGAGTGCAGCGGAAGCGGAGGAATCAG 933
QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 934 GAGATCTCAACAGCAGACTCCAGAGCGAGAGGCGCTGTTGGTGGCCAAACAGGAGGTG 993
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db 994 ATCGATAAGCTGAAGGAGGAGGCGCAGCAGCACAAGATTGTGATGGAGACCGTTCGCTG 1053
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 1054 CTGAAGGCCCAGCGGATATCTCAAGCGCGACTTCCAGGCTGAGAGGCGGCCCGGAG 1113
QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnGlnLeuGlnArgGluTyr 340
Db 1114 AAGCTGCCGAGAGAGGAGGCTCTCTGCGAGAGCAGCTGGAGCAGCTGCGAGGAGGATAC 1173
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
Db 1174 AGCAAACTGAAGGCCAGCTGTGAGGAGTCCGCCAGGATCGAGGACATGAGGAGCGCAT 1233


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; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION
; FILE REFERENCE: RTS-0191
; CURRENT APPLICATION NUMBER: US/09/972,607
; CURRENT FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 1975
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (111)....(1370)
US-09-377-607-10

Alignment Scores:
Pred. No.: 1,14e-171 Length: 1975
Score: 2105.00 Matches: 417
Percent Similarity: 99.52% Conservative: 0
Best Local Similarity: 99.52% Mismatches: 2
Query Match: 99.53% Indels: 0
DB: 10 Gaps: 0

US-09-377-795-2 (1-419) x US-09-972-607-10 (1-1975)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
DB 111 ATGAATAGGCACCTCTGGAGAGCCAACTGTGTGAGATGGTCAGGCCAGTGGTGCCCG 170
QY 21 AlaAlaSerGlnAspValLeuGlyGluGluSerProLeuGlyProAlaMetLeuHis 40
DB 171 GCACGAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCAGCCATGCTGCAC 230
QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluGlnGlu 60
DB 231 CTGCCTTCAGAACAGGCGCTCTGAGACCCCTCAGCGCTGCGTGGAGAGAAATCAAGAG 290
QY 61 LeuArgAspAlaLeuArgGlnSerAsnGlnLeuLeuArgGluArgCysGluGluLeu 80
DB 291 CTCGAGATGCCATCCGGCAGACCAACAGATTCTCGCGGAGCGCTGCGAGAGATTCTG 350
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
DB 351 CATTTCCAAAGCCAGCAGAGGAGGAGAGAGAGTCTCTCATGTGCAAGTTCCAGAGGCC 410
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysGlnLysGluGln 120
DB 411 AGGAACTGTGTGAGAGACTCGGCTGGAGAGCTCGATCTGAGAGGCGAGAGGAGCAG 470
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
DB 471 GCTCTGGGGAGGTGGAGCACCTTGAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 530
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
DB 531 TCTGTGAACCCAGGTGAGTCTCTGCTCGGGAGCTGCGAGAGAGCAGAGTCCGCTTG 590
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
DB 591 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGCGCCGCGCCAGCGAGCAG 650
QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
DB 651 GCSCGGCAGCTGAGAGTGGCGGAGGCGCTGCGAGCAGCAGCAGCAGCGGTGCGAGTGGAC 710
QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
DB 711 CAGCTGGCATGAGGCGCCAGAGCGTGGAGGCGCGCTCCGATGGAGCGCCAGCGCCGCC 770
QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
DB 771 TCGGAGGAGAGAGGAAGTGGGCCAGTTGCGAGTGGCGCTATCACCAGCTCTTCCAGAA 830
QY 241 TyrAspAsnHisIleLysSerValValGlnSerGluArgLysArgGlyMetGlnLeu 260
DB 831 TACGCAACCAACATCAAGAGCAGCGCTGTGGCAGTGGCGAAGCGAGGAATGCAGCTG 890
QY 261 GluAspLeuLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 280
DB 891 GAAGATCTCAACACAGCAGCTCCAGCAGCGCCGAGGAGGCGCTGTGGCCCAACAGAGGGTG 950
QY 281 IleAspLysLeuLysGluGluAlaGlnGlnHisLysIleValMetGluThrValProVal 300
DB 951 ATCGATAAGCTGAAGGAGGAGCGCCGAGCAGCAGCAAGATTGTGATGGAGACCGTTCGCGTG 1010
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
DB 1011 CTGAAGGCCCGAGCGGATATCTACAAGCGGACTTCCAGGCTGAGAGGCGAGGCCCGGAG 1070
QY 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGluTyr 340
DB 1071 AAGCTGGCGGAGAGAGAGCTCTCTGAGAGCAGCTGGAGCAGCTGCGAGGAGGTAC 1130
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
DB 1131 AGAAACTGAAGGCGCAGCTGTCAAGAGTCGCGCAGGATCGAGGACATGAGGAAGCGGCAT 1190
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLeuSerSerProLeuAla 380
DB 1191 GTCAGAGTCTCCAGGCGCCCTTGGCCCCCGCCCTGCTCTCTCTCTCTCTCTCTCTCTCT 1250
QY 381 LeuProSerGlnArgArgSerProGluGluProGluProGluProGluProGluProGlu 400
DB 1251 CTGCCCAGTCAGAGAGGAGGAGGCCCGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1310
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnGlnHisValMetGluCysIleGlu 419
DB 1311 CAGTATCAGGCGCCCTGATATGACACCCCTGACAGATACATGTGATGAGTGCATTGAG 1367

RESULT 7
US-10-628-841-10
; Sequence 10, Application US/10628841
; Publication No. US20040023918A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION
; FILE REFERENCE: RTS-0191
; CURRENT APPLICATION NUMBER: US/10/628,841
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/972,607
; PRIOR FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 1975
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (111)....(1370)
US-10-628-841-10

Alignment Scores:
Pred. No.: 1,14e-171 Length: 1975
Score: 2105.00 Matches: 417
Percent Similarity: 99.52% Conservative: 0
Best Local Similarity: 99.52% Mismatches: 2
Query Match: 99.53% Indels: 0
DB: 17 Gaps: 0

US-09-377-795-2 (1-419) x US-10-628-841-10 (1-1975)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
DB 111 ATGAATAGGCACCTCTGGAGAGCCAACTGTGTGAGATGGTCAGGCCAGTGGTGCCCG 170
QY 21 AlaAlaSerGlnAspValLeuGlyGluGluSerProLeuGlyProAlaMetLeuHis 40
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Db 171 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 230
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAenGlnGlu 60
Db 231 CTGCTTTTCAGAAACAGGCGCTCTCTGAGACCCCTCCAGCGCTGCTGGAGGAGNAATCAAGAG 290
Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
Db 291 CTCCGAGATGCATCCGCGAGAGCAACAGATTCTGCGGAGCGCTCGAGGAGCTTCGTG 350
Qy 81 HisPheGlnAlaSerGlnArgGluGluysGluPheLeuMetCysLysPheGlnGluAla 100
Db 351 CATTTCCAAGCCAGCAGAGGAGGAGAGAGTCTCTCATGTGCAAGTTTCCAGGAGGCC 410
Qy 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 411 AGGAACTGTGGAGAGACTCGGCTCGAGAAGCTCGATTCTGAAGAGCGCAGAGGAGCAG 470
Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
Db 471 GCTCTCGGGAGGTGGAGCACCTGAAGAGATGCCAGCAGCAGATGGCTGAGGACAGGCC 530
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerArgLeu 160
Db 531 TCTGTGAAGCCAGGTGAGCTCTCTGCTCGGGAGCTGCAGGAGAGCCAGAGTCGCTTG 590
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 591 GAGGCTGCCACTAAGGAATGCCAGGCTCTGAGGGTGGGGCGGGCGCCAGCAGCAG 650
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
Db 651 GCGGGCAGCTGGAGAGTGGAGCGGAGCGCTGCAGCAGCAGCAGCAGCTGCAGGTGGAC 710
Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 711 CAGCTGCGCATCAGGCGCCAGAGCGTGGAGCGCGCTCGCATGGAGCGCCAGCGCGCC 770
Qy 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaThrHisGlnLeuPheGlnGlu 240
Db 771 TCGAGAGGAGAGAGAGTGGCGCCAGTTGAGGTGGCTTATCACCAAGCTCTTCCAAGAA 830
Qy 241 TyrAspAsnHisIleLysSerSerValValCysSerGluArgLysArgGlyMetGlnLeu 260
Db 831 TAGCAACACCATCAGACAGCGTGTGGCAGTGGAGCGGAGCGAGGAGATTCAGCTG 890
Qy 261 GluAspLysGlnGlnLeuGlnGlnAlaGluAlaLeuValAlaLysGlnGluVal 280
Db 891 GAAGATCTCAACACAGCAGCTCCAGCAGCGCGAGGCGCTGTTGGCCAAACAGGAGGTG 950
Qy 281 IleAspLysLeuLysGlnGlnGlnGlnGlnHisIleValMetGluThrValProVal 300
Db 951 ATCGATAAGCTGAAGGAGGAGGCGGAGCAGCAGCAAGATTGTGATGGAGACCGTTCCGGTG 1010
Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 1011 CTGAGGCCAGGCGGATATCTACAGGCGGACTTCCAGGCTGAGAGGCGGCGCGGAG 1070
Qy 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnGlnArgGlyTyr 340
Db 1071 AAGCTGGCCGAGAAGAAGAGGCTCTCTGAGGAGCAGCTGGAGCAGCTGCAGAGGGAGTAC 1130
Qy 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
Db 1131 AGAAACTGAAGCCAGCTGTCAAGAGTTCGGCAGGATCGGAGACATGAGGAAGCGGCAT 1190
Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 1191 GTGAGGTCTCCAGGCGCCCTTGGCCCCCGCCCTGCTTCTCTCTCCCTTGGCC 1250
Qy 381 LeuProSerGlnArgArgSerProProGluGluProProAspPheCysCysProLysCys 400

Db 1251 CTGCCAGTCAGAGGAGGCGCCCCAGAGAGCCACCTGACTTCTGCTGCTCCCAAGTGC 1310
Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 1311 CAGTATCAGGCCCCGTGATGGAACCCCTGCAGATACATGTCATGGAGTCATTGAG 1367
RESULT 8
US-10-761-370-2
; Sequence 2, Application US/10761370
; Publication No. US20040219615A1
; GENERAL INFORMATION:
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR F
; FILE REFERENCE: WALLACH-27
; CURRENT APPLICATION NUMBER: US/10/761,370
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: US/09/646,403
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: IL 123758
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: PCT/IL99/00158
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: IL 126024
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-761-370-2
Alignment Scores:
Pred. No.: 4.57e-165 Length: 2034
Score: 2028.50 Matches: 413
Percent Similarity: 97.64% Conservative: 0
Best Local Similarity: 97.64% Mismatches: 6
Query Match: 95.91% Indels: 4
DB: 18 Gaps: 1
US-09-377-795-2 (1-419) x US-10-761-370-2 (1-2034)
Qy 1 MetAsnArgHisLeuTrrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 172 ATGAATAGGCACCTCTGGGAAGAGCCAACTGTGTGAGATGGTGCAGCCCGCTGGGCCCG 231
Qy 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 232 GCAGCAGATCAGGACGCTACTGGGCGAAGAGTCTCTCTGGGGGAAGCCAGCATGCTGCAC 291
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAenGlnG 60
Db 292 CTGCTTTCAAGACAGGCGCTCTCTGAGACCCCTCCAGCGCTGCTGGAGGAGGAATCAAGA 351
Qy 60 uLeuArgAspAlaIleArgGln-SerAsnGlnIleLeuArgGluArgCysGlu---GluL 79
Db 352 GCTCCGAGATGCCATCCGCGAGTAGCAACACAGATTCTTTCGGGAGCTGCGCAAGGGAGCT 411
Qy 79 euleuHis-PheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGln 98
Db 412 TTCTGATTTTCCAGCCAGCCAGAGGAGGAGAGGAGTTCCTCATGTGCATGTTCCAG 471
Qy 99 GluAlaArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLys 118
Db 472 GAGGCAGGAAACTGTTGGAGAGACTCGGCTCGAGAAAGCTCGATCTGAAGAGGAGCAAG 531
Qy 119 GluGlnAlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAsp 138
Db 532 GAGCAGGCTCTGCGGAGGTGGAGCACCTCAAGAGATGCCAGCAGCAGATGGCTGAGGAC 591
Qy 139 LysAlaSerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerGlnSer 158

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Db 592 AAGCCCTCTGGAAGCCCAAGTACGCTCTTCTCGGGAGCTGCAGGAGCCAGAGT 651
Qy 159 ArgLeuGluAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaAlaLaser 178
Db 652 CGCTTGGAGGCTGCCACTAAGGAATGCACAGCTCTGGAGGTCGGCCCGGGCGGCAGC 711
Qy 179 GluGlnAlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGln 198
Db 712 GAGCAGCGCGGAGCTGGAGAGTGAAGCGAGGCGCTGCAGCAGCAGCACAGCGTGCAG 771
Qy 199 ValAspGlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGln 218
Db 772 GTGACACAGCTGCGCATGCGAGGCCAGAGCTGGAGCCCGCTCCGCGTGGAGCCCGAG 831
Qy 219 AlaAlaSerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaThrHisGlnLeuPhe 238
Db 832 CGCGCCTCGGAGGAGAGAGAGAGTGGCCAGTTCAGGTCGGCTATCACAGCTCTTC 891
Qy 239 GlnGluTrpAspHisLysSerValValGlySerGluArgLysArgGlyMet 258
Db 892 CAGAATACGACACACACATCAAGAGCAGCGTGGTGGCGAGTGAGCGGAAGCGAGGAATG 951
Qy 259 GlnLeuGluAspLeuLysGlnGlnLeuGlnAlaGluAlaLeuValAlaLysGln 278
Db 952 CAGCTGGAAGATCTCACAACAGCAGCTCCAGAGCGCGAGAGGCCCTGGTGGCCAAACAG 1011
Qy 279 GluValLysLeuLysGlnGluAlaGluGlnHisLysLeuValMetGluThrVal 298
Db 1012 GAGGTGATCGATAAGCTGAAGGAGGAGGCGCGAGCAGCACAGATTGTGATGAGACCGTT 1071
Qy 299 ProValLeuLysAlaGlnAlaAspLeuLysAlaAspPheGlnAlaGluArgGlnAla 318
Db 1072 CCGGTGCTGAAGCCCGAGCGGATATCTCAAGCGGACTTCAGGCTGAGAGGCGAGGCC 1131
Qy 319 ArgGluLysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnLeuArg 338
Db 1132 CGGAGAAAGCTGGCCGAGAAGAGGAGCTCTTCAGAGCAGCTGGAGCAGCTGCAGAGG 1191
Qy 339 GluTrpSerLysLeuLysAlaSerCysGlnGluSerAlaArgLysLeuAspMetArgLys 358
Db 1192 GAGTACAGCAAACTGAAGCCAGCTCTCAGGAGTCCGCCAGGATCGGACATGAGGAAG 1251
Qy 359 ArgHisValGluValSerGlnAlaProLeuProAlaProAlaProAlaThrLysSerPro 378
Db 1252 CGCATGTCTGAGTCTCCAGGCCCCCTTGGCCCCCGCCCCCTTACCTCTCTCTCCC 1311
Qy 379 LeuAlaLeuProSerGlnArgSerProProGluGluProProAspPheCysPro 398
Db 1312 CTGGCCCTGCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1371
Qy 399 LysCysGlnTrpGlnAlaProAspMetAspThrLeuGlnHisValMetGluCysLeu 418
Db 1372 AAGTGCAGTATCAGGCCCCCTGATATGGACACCTTCAGATACATGTATGAGTGCATT 1431
Qy 419 Glu 419
Db 1432 GAG 1434
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RESULT 9

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US-10-792-063-4
; Sequence 4, Application US/10792063
; Publication No. US20040175797A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jason
; APPLICANT: Garrett-Engle, Phillip
; APPLICANT: Kan, Zhengyan
; TITLE OF INVENTION: IKBG
; FILE REFERENCE: R03-011-208PV
; CURRENT APPLICATION NUMBER: US/10792,063
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 06/452,293
; PRIOR FILING DATE: 2003-03-04
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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-063-4

Alignment Scores:
Pred. No.: 3,4e-149 Length: 1104
Score: 1840.50 Matches: 368
Percent Similarity: 87.93% Conservative: 0
Best Local Similarity: 87.83% Mismatches: 0
Query Match: 87.02% Indels: 51
DB: 18 Gaps: 1

US-09-377-795-2 (1-419) x US-10-792-063-4 (1-1104)

Qy 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 1 ATGAATAGGCACCTCTGGAGAGCCAACTGTGTGAGATGGTGCAGCCACAGTGGTGGCCCG 60
Qy 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 61 GCAGCAGATCAGGACGACTACTGGCGGAAGAGTCTCTCTGGGGGAAGCCAGCCATGCTGCAC 120
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
Db 121 CTGCCTTCAGAAACAGGCGCTCTCTGAGACCTCTCCAGCGCTCCCTGGAGGAGAAATCAAGAG 180
Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeu 80
Db 181 CTCGAGATGTCATCCGCGCAGAGCAACAGATCTCTCGCGGAGCGCTGGCAGAGGCTTCTG 240
Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
Db 241 CATTTCCAAAGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Qy 101 ArgLysLeuValGluArgLeuGlyLeuGlyLysLeuAspLeuLysArgGlnLysGln 120
Db 301 AGGAAACTGGTGGAGAGACTCGGCTCGGAGAGCTCGATCTCTGAAGAGGAGGAGGAGGAG 360
Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
Db 361 GCTCTGGGAGGAGTGGAGACCTTGAAGATGTCAGAGATGTCAGAGGAGGAGGAGGAGGAG 420
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
Db 421 TCTGTGAAAGCCCAAGGTGACGCTCTTCTCGGGGAGCTGCAGGAGAGGAGGAGGAGGAG 480
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 481 GAGCTCTCCACTAAGGAATGCCAGGCTCTGGAGGAGTGGG----- 519
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGlnValAsp 200
Db 519 ----- 519
Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 519 ----- 519
Qy 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaThrHisGlnLeuPheGlnGlu 240
Db 520 -----AGGAAAGCTGGCCAGTTCAGGTCGCTATCACCAGCTCTTCCAGAA 567
Qy 241 TyrAspAsnHisLysSerSerValValCysSerGluArgLysArgGlyMetGlnLeu 260
Db 568 TACGACAAACACATCAAGACAGCAGCGTGGTGGCGAGTGCAGGAGGAGGAGGAGGAGGAG 627
Qy 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 628 GAAGATCTCAACAGCAGGCTCCAGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 687
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; Publication No. US20030228667A1
; GENERAL INFORMATION:
; APPLICANT: SHOJI, YAMAKA
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE ENCODING A MODULATOR OF NF-KB
; FILE REFERENCE: 0660-0146-55
; CURRENT APPLICATION NUMBER: US/10/408,305
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US/09/253,701
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1874
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-408-305-2

Alignment Scores:
Pred. No.: 2,26e-147 Length: 1874
Score: 1822.50 Matches: 362
Percent Similarity: 90.93% Conservative: 19
Best Local Similarity: 86.40% Mismatches: 31
Query Match: 86.17% Indels: 7
DB: 17 Gaps: 1

US-09-377-795-2 (1-419) x US-10-408-305-2 (1-1874)

QY 1 MetAsnArgHisLeuTyrPheGlnLeuGluMetValGlnProSerGlyGlyPro 20
DB 94 ATGAACAGACCCCTCGAAGAACACAGCTGAGTGAGACGGTGCAGCCAGTGGTGCCCA 153

QY 21 AlaAlaSerGlnValLeuGluGlyGluSerProLeuGluGlyPheAlaMetLeuHis 40
DB 154 GCAGAGACCCAGGACATGCTGGGTGAGAAATCTTCTCTGGGAAGCCTGCAATGCTACAT 213

QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60
DB 214 CTGCCTTCAGAGCAGGCTACTCTCTGAGACCCCTCAGCGCTGCCTGAGAGAAATCAAGAG 273

QY 61 LeuArgAspAlaLeuArgGlnSerAsnGlnLeuLeuArgGluArgCysGluLeuLeu 80
DB 274 CTCGAGACCCCTATCCGGCAGAGCAATCAGATGCTGAGGGAACGCTGTGAGAGCTGCTG 333

QY 81 HisPheGlnAlaSerGlnArgGluGluGlyGluPheLeuMetCysLysPheGlnGluAla 100
DB 334 CATTTCCAGCTCAGCCAGCGGAGAGAGAGGTTCTTATGTGCAATTCAGAGAACCC 393

QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
DB 394 CGGAAGCTGTGGAGAGACTGAGCTTGGAGAAGCTTGATCTTCGGAGTCAGAGGGAACAG 453

QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
DB 454 GCCTTAAGAGGTGGAGCACTGGAAGAAATGCCAACAGCAGATGCTGAGGACAAGGCC 513

QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerGlnSerArgLeu 160
DB 514 TCTGTGAAGCTCAGGTGACATCATTTGCTCGAGAACTCCAGAGAGCCAGAGCGGTG 573

QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaAlaSerGluGln 180
DB 574 GAGCTGCCACCAAGATCGGAAGCTTTAGAGGAAGGATTCGAGCAGATTAGTGAGCAG 633

QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
DB 634 GTCAGACAGCTGGAGATGAGCGGGAGGTGCTACAGCAGCAGCAGCAGCTCAGGTGAC 693

QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaLeuArgMetGluArgGlnAlaAla 220
DB 694 CAGCTGCGTATGCAGAACACAGAGCGTGGAGGTGCTTGGCAATGGAGCGGCGAGCTGCT 753

QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnPheGlnGlu 240
DB 1 GAGCTGCGTATGCAGAACACAGAGCGTGGAGGTGCTTGGCAATGGAGCGGCGAGCTGCT 753

; US-09-377-795-2 (1-419) x US-10-792-063-8 (1-486)
QY 258 MetGlnLeuGluAspLeuLysGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLys 277
DB 1 ATGAGCTGGAAGATCTCAACAGCAGCTCCAGAGCGGAGGAGGCGCTGCTGGTCCCAAA 60
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Db 754 TCAGAGGAGAAGCGGAAGCTGGCTCAGTTGCAGGAGCCCTATCACCACACTCTTCCAAGAC 813
QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 814 TACGACAGCCACATTAAGAGCAGC-----AAGGCGATGCGAGCTG 852
QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 853 GAAGATCTGAGGCAACAGCTCCAGCAAGCTGAGGAGGCCCTGTTAGTGAATG 912
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db 913 ATTGATAAGCTGAAAGAGAGGAGCTGAGCAGCAAGATTTGTATGAGAGACTGTGCCAGTC 972
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 973 TTGAAGGCCCCAGCGGATATCTACAGGCTGACTTCCAGCTGAGAGGATGCCCGGAG 1032
QY 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnLeuGlnGlnLeuGlnArgGluTyr 340
Db 1033 AAGCTGTGGAGAAAGAGAGTATTTGAGGAGCAGCTGAGCAGCTGCAGCGCAGATTTC 1092
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
Db 1093 AACAGCTGAAAGTGGCTGCCATGATGACCCAGATTGAGGATATGAGGAAGCGGCAT 1152
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 1153 GTAGAGACTCCCGACGCTCTTTACTCCTGCTCCAGCTCACCACCTCTTTCATTTGGCC 1212
QY 381 LeuProSerGlnArgArgSerProProGluGluProProAspPheCysCysProLysCys 400
Db 1213 TTGTCCACACCGAGGAGGCCCTCCAGAACCTCTCTGACTTCTGTGTGCGAAGTGC 1272
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 1273 CAGTATCAGGCTCTGTATATGGACACTTACAGATACATGTCTATGAGTGCATAGAG 1329

RESULT 12
US-10-792-063-8
; Sequence 8, Application US/10792063
; Publication No. US20040175797A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jason
; APPLICANT: Garrett-Engle, Phillip
; APPLICANT: Kan, Zhengyan
; TITLE OF INVENTION: IKKKG
; FILE REFERENCE: R03-011-208PV
; CURRENT APPLICATION NUMBER: US/10/792,063
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 06/452,293
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-063-8

Alignment Scores:
Pred. No.: 2,33e-62 Length: 486
Score: 827.00 Matches: 162
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 39.10% Indels: 0
DB: 18 Gaps: 0

US-09-377-795-2 (1-419) x US-10-792-063-8 (1-486)
QY 258 MetGlnLeuGluAspLeuLysGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLys 277
Db 1 ATGAGCTGGAAGATCTCAACAGCAGCTCCAGAGCGGAGGAGGCGCTGCTGGTCCCAAA 60
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QY 278 GlnGluValIleAspLysLeuLysGluAlaGluGlnHisLysIleValMetGluThr 297
DB 61 CAGGAGGTGATCGATAGCTGAAGGAGAGCCGAGCAGACAGATTGTGATGGAGACC 120
QY 298 ValProValLeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGln 317
DB 121 GTTCCGGTGTGAAGGCCAGCCAGCGGATATCTACAAGGCGGACTTCCAGGCTGAGAGGCAG 180
QY 318 AlaArgGluLysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnGlnGlnGln 337
DB 181 GCCCGGAGAGCTGGCCGAGAGAGAGAGCTCTCGAGGAGCAGCTGGAGCGACTGCAG 240
QY 338 ArgGluTyrSerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArg 357
DB 241 AGGAGGTACAGCAAACTGAAGGCCAGCTGTGAGAGTGGCCAGGATCGAGGACATGAGG 300
QY 358 LysArgHisValGluValSerGlnAlaProLeuProProAlaProAlaTyrLeuSerSer 377
DB 301 AAGCGGCATGTGAGGTCTCCAGGCCCTTGGCCGCCCTTGGCCGCCCTTACCTCTCTCTCT 360
QY 378 ProLeuAlaLeuProSerGlnArgArgSerProGluGluProProAspPheCysCys 397
DB 361 CCCTGGCCCTGGCCAGCAG 420
QY 398 ProLysCysGlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCys 417
DB 421 CCCAAGTGCAGTATCAGGCCCTTGATATGAGACACCTCGCATATGTCATGGAGTGC 480
QY 418 IleGlu 419
DB 481 ATTGAG 486

RESULT 13

US-10-792-063-6

; Sequence 6, Application US/10792063

; Publication No. US20040175797A1

; GENERAL INFORMATION:

; APPLICANT: Johnson, Jason

; APPLICANT: Garrett-Engle, Phillip

; APPLICANT: Kan, Zhengyan

; TITLE OF INVENTION: IKRG

; FILE REFERENCE: R03-011-208PV

; CURRENT APPLICATION NUMBER: US/10/792,063

; CURRENT FILING DATE: 2004-03-03

; PRIOR APPLICATION NUMBER: US 06/452,293

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 483

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-792-063-6

Alignment Scores:

Pred. No.:	2,72e-56	Length:	483
Score:	756.50	Matches:	159
Percent Similarity:	63.49%	Conservative:	1
Best Local Similarity:	63.10%	Mismatches:	0
Query Match:	35.77%	Indels:	92
DB:	18	Gaps:	1

US-09-377-795-2 (1-419) x US-10-792-063-6 (1-483)

QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
DB 1 ATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGTTGTCAGATGTTGTCAGCCCG 60
QY 21 AlaAlaAspGlnAspValLeuGluGluSerProLeuGlyLysProAlaMetLeuHis 40
DB 61 GCAGCAGATCAGGACGATCTGGGCGAAGAGTCTCTCTGTCGGGAAGCAGCCATGCTGCAC 120

QY 41 LeuProSerGluGlnGlnAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
DB 121 CTGCTTTAGAACAGGCGCTCTCTGAGACCTCTCAGCGCTGCTTGGAGGAGATCAAGAG 180
QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80
DB 181 CTCCGAGATGCCATCCGGCAGAGCAACAGATTCTCGCGAGCGCTCCGAGGAGCTTCTG 240
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
DB 241 CATTTCCAGCCAGCCAGAGGAGGAGAGAGTTCCTCATGTGCAAGTTTCCAGGAGGCC 300
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnGln 120
DB 301 AGAAACTGTTGGAGAGACTCGGCCCTGGAGAGCTCGATCTGAAGAGGAGAGGAGCAG 360
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
DB 361 GCTCTCGGAGGAGTGGAGCACCTGAAGAGATGCCAG----- 396
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerArgLeu 160
DB 396 ----- 396
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
DB 396 ----- 396
QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
DB 396 ----- 396
QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
DB 396 ----- 396
QY 221 SerGluGluLys-ArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnG 240
DB 397 -----CAGGAGGAGAGCTGGCCAGCTTGAGGTGGCTATCACCAGCTCTTCCAGA 447
QY 240 uTyrAspAsnHisIleLysSerSerValValGly 251
DB 448 ATACGACCAACCATCATCAGAGCAGCGCTGGTGGGC 481

RESULT 14

US-09-863-049A-1

; Sequence 1, Application US/09863049A

; Publication No. US20030032055A1

; GENERAL INFORMATION:

; APPLICANT: Kenwick, Sue J.

; APPLICANT: Nelson, David L.

; APPLICANT: Aradhya, Swaroop

; APPLICANT: D'Urso, Michele

; APPLICANT: Woffendin, Hayley

; APPLICANT: Munnich, Arnold

; APPLICANT: Smahi, Asmae

; APPLICANT: Israeli, Alain

; APPLICANT: Poustka, Annemarie

; APPLICANT: Lewis, Richard A

; APPLICANT: Levy, Moise

; APPLICANT: Heiss, Nina

; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Def

; FILE OF INVENTION: NFKAPPA B (NF-KB) Activation

; FILE REFERENCE: HO-P01961US1

; CURRENT APPLICATION NUMBER: US/09/863,049A

; CURRENT FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: US 60/206,223

; PRIOR FILING DATE: 2000-05-22

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 23106

; TYPE: DNA

i ORGANISM: Human

US-09-863-049A-1

Alignment Scores:

Pred. No.: 1.72e-39 Length: 23106
Score: 584.50 Matches: 246
Percent Similarity: 18.18% Conservative: 0
Best Local Similarity: 18.18% Mismatches: 1
Query Match: 27.64% Indels: 1107
DB: 10 Gaps: 5

US-09-377-795-2 (1-419) x US-09-863-049A-1 (1-23106)

Qy 173 ArgAlaArgAlaAlaSerGluGlnAlaArgGlnLeuGluSerGluArgGluAlaLeuGln 192
Db 18141 AGGCCCGGGCGGCCAGCGAGCGAGGCGCGCGAGCTGGAGAGTGAAGCGCTGCGAG 18200
Qy 193 GlnGlnHisSerValGlnValAspGlnLeuArgMetGlnGlyGlnSerValGluAlaAla 212
Db 18201 CAGCAGCACAGCGTGCAGGTGGACCGAGCTGGCATCGCAGGGCCAGAGCGTGGAGCGCGG 18260
Qy 213 LeuArgMetGluArgGlnAlaAlaSerGluGluLys----- 224
Db 18261 CTCGCGATGAGCGCCAGGCGCGCTCGAGGAGAGTGAAGTCAAGCGGGCGGCGCGCA 18320
Qy 224 ----- 224
Db 18321 CCGCAGGCTGTGGTCTTACACTTGATCTTAGCCGAAAGGCTGAGAGTGCAGGTCOA 18380
Qy 224 ----- 224
Db 18381 TGGTCTCTTCTGCTTCTGAGGACTCTTTCAGATTCTGCGTGTGGCTGTGGGCCCATCT 18440
Qy 224 ----- 224
Db 18441 GTCCCTTAGCCTTGCTAACGGTAGAGCGACCATGATGACACCGGTTTGTCTTTGATAC 18500
Qy 224 ----- 224
Db 18501 AGTCATGCCATCTGCTCTCCAGACACAGTTTCACTGCGTGTCCACAGTGGCCTTTTGTG 18560
Qy 224 ----- 224
Db 18561 TAGTTTTTTTCTAGCCACTAGGTCAATCAGGGGACTTGTCTTTAAACCCCTTCTAG 18620
Qy 224 ----- 224
Db 18621 GCCAGGTGTGTGGTCAAGCCTGTAAATCCCAACACTTTGGAGGCCAAAGTGGGTAGAT 18680
Qy 224 ----- 224
Db 18681 GGCTTAAGCCCGGAGTTCCAGACACCGCTGGGCAACAGAAAGACAAATAATACCCC 18740
Qy 224 ----- 224
Db 18741 CAAACCCCGCTTACCAGCATCCAAATCTGGAGCCTCAGGTTCCTGTCTTGGCGTGCC 18800
Qy 224 ----- 224
Db 18801 TTTTCAGTCTCCTTTAATCTAGAACAGTTCCCGCTGCTTTCTGAGCTGTTGTGAAGTTC 18860
Qy 224 ----- 224
Db 18861 ACAGTTTGAAGAGTGCAGGTAGTTCCATTTGTAATTAATTAATTAATTTCAAGACAGGG 18920
Qy 224 ----- 224
Db 18921 TCTTGCTCTACCGTCCAGGCTGGAGTGCAGTGGCATAAATCTCGGCTTACTGTACCTCCG 18980
Qy 224 ----- 224
Db 18981 CCTCTGGTCTCAAGCGATCTCCAGGTAGCTGGGACTATAGGCGGCGAGCACACC 19040

Qy 224 ----- 224
Db 19041 TGGCTAATTTTGGCATTTTGGTAGAGTGGCGTTTCTCTATGTTGCCCGGCTGTCTT 19100
Qy 224 ----- 224
Db 19101 GAACTCTGAGCTCAAGCGATCCTCCTCGCTTGGCTTCTCAAAAGTGTGGGATTTAGGC 19160
Qy 224 ----- 224
Db 19161 GTAGCCACCGCTCTGCGCGGATTTTATTATAAATTAATAAATACTAGCTTTTAGGA 19220
Qy 224 ----- 224
Db 19221 AAAGATATTAACTGCTGGTGACGACGCCACCAAGGCTGCTTTAGAGTTGACGCGCTC 19280
Qy 224 ----- 224
Db 19281 AGGAGTCTCACACAGCCTTGGAGACCCCATTCAGGCTGTGATGCGAGGGAGGAAG 19340
Qy 224 ----- 224
Db 19341 GAAGGGGTAGAGTTGGAAGCAGCAGCAGCCTGGCTGGACTGGCATGAGGTGTTCTC 19400
Qy 225 ----- 236
Db 19401 CAGCAAAAGTCCCTTTCTCAGGAGGAAGCTGGCCCAAGTTGCAGGTGGCCTATCACCA 19460
Qy 237 LeuPheGlnGluTyrAspAsnHisIleLysSerValValGlnValAlaTyrHisGln 256
Db 19461 CTCCTCAAGAATACGACACCAACATCAAGAGCAGCTGGTGGGCGAGTGCAGCGGAAGCA 19520
Qy 256 ----- 256
Db 19521 GTAGTGCACCACTGGGGCTCTTAGGGCTGGCCTTTCCTCTCTCCCGTGGCCT 19580
Qy 256 ----- 256
Db 19581 GAACCTTGAGAAATGGTCTCCTCCTTAGACTTGGCTTAGACCTGTGTGAGGTGCAGCTGC 19640
Qy 256 ----- 256
Db 19641 GACAGCTCAGGGAAGCTGTGGGAGATGGCAACCCAGGATGTTGCTCTCAGGAGTGTCA 19700
Qy 256 ----- 256
Db 19701 GCAGGCCATCTTAATGGGGGCTGGGCGCAGAGCCTTGGGGTGTCTCCCTCTGTGGGGCTGG 19760
Qy 256 ----- 256
Db 19761 GGAGCTCTTGTCTCCATGGACATTCCTCTTTCAGAGCATCGCCATCTGGCACCTGGGCTC 19820
Qy 256 ----- 256
Db 19821 AGCTTCCCGCAAGCAAGTAAGCCGACAGCAITTCACCCAGTGTGTGGCTGGGAGCC 19880
Qy 256 ----- 256
Db 19881 TTTTCTAGTTTGTCTCATCAGACCTAAAGCTGGGGTGCAGTTTGTCTAGTATCATATTT 19940
Qy 256 ----- 256
Db 19941 TAGCAGGACACCGTCAATCGTAAGTGTACCCAGAGGAGATTTATAAGGACAAAGCTGAA 20000
Qy 256 ----- 256
Db 20001 GCCAGGTCAATGGGGAAGATTAGCTACAAACTGCGCACTTAATCTCTGGAGGGGCG 20060
Qy 256 ----- 256
Db 20061 GTTGGTGGGTGTGTCTGTGTGTCTCAGGGGGCTGGAGATGCTGCTGGGAGGAGTG 20120
Qy 256 ----- 256

FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 84
LENGTH: 2803
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (10)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (50)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (517)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (572)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1926)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-298-84

Alignment Scores:
Pred. No.: 2,14e-28 Length: 2803
Score: 443.00 Matches: 85
Percent Similarity: 94.51% Conservative: 1
Best Local Similarity: 93.41% Mismatches: 5
Query Match: 20.95% Indels: 0
DB: 9 Gaps: 0

US-09-377-795-2 (1-419) x US-09-925-298-84 (1-2803)

Qy	1	MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro	20
Db	284	ATGATAGGACCTCTGGAGAGCCCACTGTGTGAGATGGTGCAGCCCGAGTGGCCCG	225
Qy	21	AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis	40
Db	224	GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGAAGCCAGCCATGCTGCAC	165
Qy	41	LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu	60
Db	164	CTGCCTTCAGAACAGGGCGCTCTGAGACCCCTCCAGCGTGGCTGAGGAGATCAAGAG	105
Qy	61	LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeu	80
Db	104	CTCGAGATCCATCCGGCAGACACACAGATTCTTTCGGGACCTTGGCAGAGNTTTTG	45
Qy	81	HisPheGlnAlaSerGlnArgGluGluLysGlu	91
Db	44	SATTTCCAGCCAGCCAGAGGAGGAGGAGGAT	12

Search completed: February 9, 2005, 06:53:53
Job time : 1660 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 9, 2005, 01:01:13 ; Search time 5944 Seconds
(without alignments)
3415.669 Million cell updates/sec

Title: US-09-377-795-2

Perfect score: 2115

Sequence: 1 MNRHLWKSQCEVQPSGGP.....COYQAPDMDTLQIHVMECIE 419

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=genembl -QFWT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEADPS12B=550 -MINLEN=0 -MAXLEN=2000000000
-USER=US03377795 @CGN 1 4200 @runat_07022005_112551_12117 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

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2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
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8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2115	100.0	1966	9 BC000299	BC000299 Homo sapi
2	2115	100.0	1990	9 BC050612	BC050612 Homo sapi
3	2115	100.0	1994	9 AF074382	AF074382 Homo sapi
4	2115	100.0	2009	6 BD135431	BD135431 Receptor

5	2115	100.0	2009	6	CQ867779	Sequence
6	2115	100.0	2009	6	AR534835	Sequence
7	2115	100.0	2009	6	AX017214	Sequence
8	2115	100.0	2035	9	AF091453	Homo sapi
9	2115	100.0	2071	9	BC012114	Homo sapi
10	2115	100.0	2073	9	AY114157	Homo sapi
11	2115	100.0	2121	9	AF261086	Homo sapi
12	2105	99.5	1975	9	AF062089	Homo sapi
13	2028.5	95.9	2034	6	BD135432	Receptor
14	2028.5	95.9	2034	6	CQ867780	Sequence
15	2028.5	95.9	2034	6	AR534836	Sequence
16	2028.5	95.9	2034	6	AX017215	Sequence
17	1848.5	87.4	1239	10	AY392762	Rattus no
18	1828.5	86.5	1798	10	AF513109	Mus muscu
19	1828.5	86.5	2250	10	AY112937	Mus muscu
20	1822.5	86.2	1748	10	AF069542	Mus muscu
21	1822.5	86.2	1874	6	AR454143	Sequence
22	1813	85.7	2282	10	BC021431	Mus muscu
23	1799	85.1	2175	4	BTA414557	Bos tauru
24	1576.5	74.5	1666	9	AK000593	Homo sapi
25	1414	66.9	2038	6	AX781112	Sequence
26	1149.5	54.3	716	9	AY429546	Homo sapi
27	922.5	43.6	600	9	AY429547	Homo sapi
28	601	28.4	137217	2	HS211110	Otolemur
29	594	28.1	202213	2	AC148902	Macaca mu
30	589.5	27.9	148309	2	AC146529	Macaca mu
31	589.5	27.9	178507	2	AC146312	Macaca mu
32	589	27.8	136551	2	AC149258	Papio anu
33	589	27.8	165013	2	AC149865	Papio anu
34	584.5	27.6	23106	9	HS217178	Homo sapi
35	579.5	27.4	126566	9	AC144385	Pan trogl
36	579.5	27.4	155221	2	AC145688	Pan trogl
37	576	27.2	142017	2	HS196818	Homo sapi
38	551	26.1	147234	9	AF277315	Homo sapi
39	551	26.1	147234	9	AF277315	Homo sapi
40	551	26.1	160656	2	AL592072	Homo sapi
41	506	23.9	2075	5	BC055628	Danio rer
42	476.5	22.5	2536	5	BC063986	Danio rer
43	453.5	21.4	40000	10	AF326207	Mus muscu
44	453.5	21.4	188873	2	AC073658	Mus muscu
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ALIGNMENTS

RESULT 1	BC000299	1966 bp	linear
LOCUS	Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma, mRNA (cdna clone MGC:8374 IMAGE:2820134), complete cds.		
DEFINITION	BC000299.2 GI:33875269		
ACCESSION	BC000299		
VERSION	BC000299.2		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1966)		
	Klausner,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Altschul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,		

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 2 (bases 1 to 1966)
 Strausberg, R.
 Direct Submission
 Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 19, 2003 this sequence version replaced gi:12653066.
 Contact: MGC help desk
 Email: cgapbe-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nri.nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mascian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 1 Row: c Column: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361093.

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 Query Match: 100.00% Indels: 0
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VERSION AF074382.1 GI:3641279
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REFERENCE 1 (bases 1 to 1994)
AUTHORS Rothwarf,D.M., Zandi,E., Natoli,G. and Karin,M.
TITLE IKK-gamma is an essential regulatory subunit of the IkappaB kinase
complex
JOURNAL Nature 395 (6699), 297-300 (1998)
MEDLINE 98421680
PUBMED 9751060
REFERENCE 2 (bases 1 to 1994)
AUTHORS Rothwarf,D.M., Zandi,E., Natoli,G. and Karin,M.
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REFERENCE
1 (bases 1 to 209)
AUTHORS
Wallach,D., Kovalenko,A., Horwitz,M.S. and Li,Y.
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Receptor function regulator for TNF/NGF receptor family and other proteins
JOURNAL
Patent: JP 2002506644-A 1 05-MAR-2002;
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ACCESSION CQ867779
VERSION CQ867779.1
KEYWORDS GI:51997898
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Wallach,D. and Kovalenko,A.
TITLE Modulators of receptors of the tnfrngf receptor family
JOURNAL Patent: EP 1454985-A 1 08-SEP-2004;
FEATURES YEDA RESEARCH & DEVELOPMENT COMPANY, LTD. (IL)
source Location/Qualifiers
1. 2009
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US-09-377-795-2 (1-419) x CQ867779 (1-2009)
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Wallach,D. and Kovalenko,A.

Modulators of receptors of the tnfrngf receptor family

Patent: EP 1454985-A 1 08-SEP-2004;

YEDA RESEARCH & DEVELOPMENT COMPANY, LTD. (IL)

Location/Qualifiers

1. 2009

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Wallach, D., Kovalevskaya, A., Li, Y., and Horwitz, M.S.
TITLE Modulators of the function of receptors of the tnfrngf receptor family and other proteins
JOURNAL Patent: WO 9947672-A 1 23-SEP-1999;
WALLACH DAVID (IL); YEDA RES & DEV (IL); KOVALENKO ANDREI (IL);
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REFERENCE 1 (bases 1 to 2035)
AUTHORS Jin, D.Y., and Jeang, K.T.
TITLE Isolation of full-length cDNA and chromosomal localization of human NF-kappaB modulator NEMO to Xq28
JOURNAL J. Biol. Chem. 274 (25), 17402-17405 (1999)
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PUBMED 10087442
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AUTHORS Jin, D.Y., Giordano, V., Kibler, K.V., Nakano, H., and Jeang, K.T.
TITLE Role of adapter function in oncoprotein-mediated activation of NF-kappaB. Human T-cell leukemia virus type I Tax interacts directly with IkappaB kinase gamma
J. Biol. Chem. 274 (25), 17402-17405 (1999)
MEDLINE 99292691

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 AUTHORS Jin, D. Y.
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 JOURNAL Submitted (13-SEP-1998) LMM, NIAID/NIH, 9000 Rockville Pike, Bethesda, MD 20892-0460, USA
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 REFERENCE 1 (bases 1 to 2071)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
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Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbe, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, K., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smalhus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences (26), 16899-16903 (2002)

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

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2 (bases 1 to 2071)

Direct Submission

Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361093.

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Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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US-09-377-795-2 (1-419) x BC012114 (1-2071)

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 QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
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RESULT 10

AY114157
 LOCUS AY114157 Homo sapiens inhibitor of kappaB kinase gamma (IKBK) mRNA, complete cds.
 ACCESSION AY114157
 VERSION AY114157.1 GI:31321969
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2073)
 Perelygin,A.A. and Perelygina,L.M.
 Ikbk gene modulates the herpes virus susceptibility in mice
 JOURNAL Unpublished
 2 (bases 1 to 2073)
 Perelygin,A.A. and Perelygina,L.M.
 Direct Submission
 Submitted (17-MAY-2002) Biology, Georgia State University, 24 Peachtree Center Ave., Atlanta, GA 30303, USA
 JOURNAL Location/Qualifiers
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gene

CDS

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Qy	341	SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis	360
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Qy	381	LeuProSerGlnAlaArgSerProProGluGluProProAspPheCysCysProLysCys	400
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LOCUS	2121 bp mRNA linear
DEFINITION	Homo sapiens NF-kB essential modulator NEMO mRNA, complete cds.
ACCESSION	AF261086
VERSION	AF261086.1 GI:9802303

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      Ye.Z. and Connor,J.R.
    TITLE
      cDNA cloning by amplification of circularized first strand cDNAs
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    JOURNAL
      Biochem. Biophys. Res. Commun. 275 (1), 223-227 (2000)
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    AUTHORS
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      Ye.Z. and Connor,J.R.
    TITLE
      Direct Submission
    JOURNAL
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      Hershey, PA 17033, USA
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DEFINITION Receptor function regulator for TNF/NGF receptor family and other
proteins.
ACCESSION BD135432
VERSION BD135432.1 GI:23230377
KEYWORDS JP 2002506644-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2034)
AUTHORS Wallach,D., Kovalenko,A., Horwitz,M.S. and Li,Y.
TITLE Receptor function regulator for TNF/NGF receptor family and other
proteins
JOURNAL Patent: JP 2002506644-A 2 05-MAR-2002;
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PN JP 2002506644-A/2
PD 05-MAR-2002
PF 18-MAR-1999 JP 2000536855
PR 19-MAR-1998 IL 123758,01-SEP-1998 IL 126024 PI
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A61P35/00,
PC C07K14/47,C07K16/18,C12N1/21,C12P21/02//C07K14/525,C07K14/715,
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CC Receptor function regulator for TNF/NGF receptor family and
other proteins
FH Key 1..2034
FT source 1..2034
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Best Local Similarity: 97.64% Mismatches: 6
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JOURNAL Patent: US 6734174-A 2 11-MAY-2004;
FEATURES Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 3,26-105 Length: 2034
Score: 2028.50 Matches: 413
Percent Similarity: 97.64% Conservative: 0
Best Local Similarity: 97.64% Mismatches: 6
Query Match: 95.91% Indels: 4
DB: 6 Gaps: 1

US-09-377-795-2 (1-419) x AR534836 (1-2034)

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|||
DB 1252 CGGCATGTGAGGCTCTCCAGGCCCCCTTGGCCCCCGCCCTGCTCTCTCTCTCTCTCT 1311
QY 379 LeuAlaLeuProSerGlnArgSerProGluGluProProAspPheCysCysPro 398
|||
DB 1312 CTGGCCCTGCCAGCCAGAGGAGGAGCCCCCGGAGGAGCCACTGACTTCTGCTGTCTCT 1371
QY 399 LysCysGlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIle 418
|||
DB 1372 AAGTGGCAGTATCAGGCCCCCTGATATGGACACCCCTGCAGATACATGTCTATGAGTGCATT 1431
QY 419 Glu 419
|||
DB 1432 GAG 1434
```

Search completed: February 9, 2005, 05:09:26
Job time : 5974 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 8, 2005, 22:35:13 ; Search time 725 Seconds
(without alignments)

3421.202 Million cell updates/sec

Title: US-09-377-795-2

Perfect score: 2115

Sequence: 1 MNRHLWKSQCEVQPSGGP.....COVQAPDMDTLQIHVMECIE 419

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model -DSV=xlh
-Q=/cgn2_1/USPTO_spool/US09377795/runat_07022005_112550_12108/app_query.fasta 1.583
-DB=N Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09377795 @CGN 1.1 644 @runat_07022005_112550_12108 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_16Dec04:*

1:	Geneseqn1980s:*
2:	Geneseqn1990s:*
3:	Geneseqn2000s:*
4:	Geneseqn2001as:*
5:	Geneseqn2001bs:*
6:	Geneseqn2002as:*
7:	Geneseqn2002bs:*
8:	Geneseqn2003as:*
9:	Geneseqn2003bs:*
10:	Geneseqn2003cs:*
11:	Geneseqn2003ds:*
12:	Geneseqn2004as:*
13:	Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2115	100.0	1967	13	ADQ87415 Human tum
2	2115	100.0	1967	13	ADQ86456 Human tum
3	2115	100.0	1994	3	AAC81426 Human I-k
4	2115	100.0	1994	3	AAA35027 Human ade
5	2115	100.0	1994	3	AAF21149 Human low

6	2115	100.0	1994	8	ADA44705
7	2115	100.0	1994	10	ABZ96843
8	2115	100.0	1994	10	ABV75393
9	2115	100.0	1994	11	ABD20692
10	2115	100.0	2009	2	ACD207513
11	2115	100.0	2035	9	ACD23012
12	2115	100.0	8631	3	AAA35028
13	2115	100.0	8631	3	AAF21150
14	2115	100.0	8631	10	ABZ96844
15	2115	100.0	8631	11	ABD20693
16	2105	99.5	1260	12	ADK71964
17	2105	99.5	1975	8	ADA44712
18	2028.5	95.9	2034	2	AAZ07514
19	1840.5	87.0	1104	13	ADSI17862
20	1822.5	86.2	1874	10	ADC36537
21	1822.5	86.2	1874	12	ADI61940
22	1822.5	86.2	1874	12	ADI29002
23	1822.5	86.2	1874	13	ADI61943
24	1414	66.9	2038	10	ADF82713
25	827	39.1	486	13	ADSI17866
26	756.5	35.8	483	13	ADSI17864
27	584.5	27.6	23106	9	ACD23011
c	443	20.9	2803	3	AAF21697
29	436.5	20.6	1925	12	ADO43193
30	436.5	20.6	2076	12	ADO43195
31	430.5	20.4	1752	12	ADP80916
32	430.5	20.4	2023	12	ADO43191
33	420.5	19.9	1734	12	ADLI14949
34	420.5	19.9	1856	9	ACF03997
35	420.5	19.9	1856	12	ADO43185
36	420.5	19.9	2008	9	ACF03998
37	420.5	19.9	2008	12	ADO43187
38	420.5	19.9	2077	9	ACF03996
39	420.5	19.9	2077	12	ADO43183
40	420.5	19.9	2108	10	ADL24738
41	420.5	19.9	2139	10	ADLI15031
42	420.5	19.9	2139	12	ADP13343
43	420.5	19.9	2139	13	ADR24267
44	420.5	19.9	2327	13	ADR14212
45	420.5	19.9	2327	13	ADP23351

ALIGNMENTS

RESULT 1
ADQ87415
ID ADQ87415 standard; cDNA; 1967 BP.

XX ADQ87415;

XX 07-OCT-2004 (first entry)

XX Human tumour-associated antigenic target (TAT) cDNA sequence #4292.

XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

XX WO2004060270-A2.

XX 22-JUL-2004.

XX 15-OCT-2003; 2003WO-US029126.

XX 18-OCT-2002; 2002US-0418988P.

XX (GETH) GENENTECH INC.

XX (WUTD/) WU T D.

XX (ZHOU/) ZHOU Y.

XX Wu TD, Zhou Y;

WPI; 2004-534300/51.

New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.

Claim 1; SEQ ID NO 4292; 5504pp; English.

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) - (c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

Sequence 1967 BP; 409 A; 581 C; 629 G; 348 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No.:	8.66e-153
Score:	2115.00
Length:	1967
Matches:	419
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0
DB:	13

US-09-377-795-2 (1-419) x ADQ87415 (1-1967)

QY	1	Met	Asn	Arg	His	Leu	Trp	Lys	Ser	Gln	Leu	Cys	Glu	Met	Val	Gln	Pro	Ser	Gly	Gly	Pro	20
DB	141	AT	GA	AT	GG	CAC	CT	CG	AA	GAG	CA	CA	CT	GT	GAG	AT	GT	CG	AC	CC	CAG	200
QY	21	Ala	Ala	Asp	Gln	Asp	Val	Leu	Gly	Glu	Glu	Ser	Pro	Leu	Cys	Pro	Ala	Met	Leu	His	40	
DB	201	GC	AG	CAG	AT	CAG	GCT	ACT	GGG	CA	AG	CT	CT	CT	GGG	AA	GC	AC	CC	AT	GT	260
QY	41	Leu	Pro	Ser	Glu	Gln	Gly	Val	Ala	Pro	Glu	Thr	Leu	Gln	Arg	Cys	Leu	Glu	Glu	Asn	Gln	60
DB	261	CT	GC	CT	T	CAG	AA	CAG	GG	GC	CT	CT	CG	AC	CT	CC	AG	CG	CT	CG	AG	320
QY	61	Leu	Arg	Asp	Ala	Ile	Arg	Gln	Ser	Asn	Gln	Ile	Leu	Arg	Glu	Arg	Cys	Glu	Glu	Leu	Leu	80
DB	321	CT	CG	AG	AT	GC	AT	CGG	CAG	CA	CA	GAT	CT	CGG	GAG	CG	CT	CG	CAG	AG	CT	380

RESULT 2

RESOLUTION
ADQ86256

ID ADQ86256 standard; cDNA; 1967 BP.

XX

341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
 1169 AGCAAACTGAAGCCACCTGTCTCAGGAGTCCGCCAGGATCGAGACATGAGGAGCGCAT 1228
 361 ValGluValSerGlnAlaProLeuProProAlaProAlaProAlaProAlaProLeuAla 380
 1229 GTGAGGTCTCTCCAGGCCCTTGGCCCGCCCTTACCTCTCTCCCTGGCC 1288
 381 LeuProSerGlnArgArgSerProProGluGluProProAspPheCysCysProLysCys 400
 1289 CTGCCAGCCAGAGGAGGCCCGCCGAGAGCCCTGACTTCTCTCTCCAGATGC 1348
 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
 1349 CAGTATCAGGCCCTGATATGGACACCCCTGCAGATACATCTCATGGATGCTTGG 1405

RESULT 4
 AAA35027
 ID AAA35027 standard; DNA; 1994 BP.
 XX
 AC AAA35027;
 XX
 XX 28-JUL-2000 (first entry)
 DT
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2716.
 XX
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antasthmatic; cyostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 XX 03-AUG-1999; 99WO-US017712.
 PF
 XX 03-AUG-1998; 98US-0095212P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 PI
 XX WPI; 2000-205971/18.
 DR
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 PT
 XX Disclosure; Page 968-969; 1343pp; English.
 PS
 XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antisthmatic, cyostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the

CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.8e-153 Length: 1994
 Score: 2115.00 Matches: 419
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 3
 US-09-377-795-2 (1-419) x AAA35027 (1-1994)
 QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
 DB 149 ATGAATAGGCACCTCTGGAAAGAGCCCAACTGTGTGAGATGGTGAGCCCATGGTGGCCG 208
 QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
 DB 209 GCAGCAGATCAGGACGCTACTTGGGCGAAGAGTCTCTCTGGGGGAAGCAGCAGCATGCTGCAC 268
 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
 DB 269 CTCCTTTCAGAACAGGGCGCTCTGAGACCCCTCAGCGCTGCTGGAGGAGATCAAGAG 328
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
 DB 329 CTCGAGATGCCATCCGCGCAGACCAACAGATTCTCGGGAGCGCTGCGAGGAGCTTCTG 388
 QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
 DB 389 CATTTCCAAAGCCAGCCAGAGGGAGGAGAGTCTCTCATGTGCAAGTTCCAGGAGGCC 448
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
 DB 449 AGGAACCTGGTGAGAGACTCGGCGCTGGAGAAAGCTCGATCTGAAGAGGCGAAGAGGACG 508
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
 DB 509 GCTCTGCGGGAGGTGGAGCACCTGAAAGAGATGCCAGCAGCAGATGCTGAGGACAGGCC 568
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
 DB 569 TCTGTAAAGCCAGGTGACGCTCTTGTCTCGGGAGCTGCGAGGAGCAGCAGAGTCGCTTG 628
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
 DB 629 GAGGCTGCCACCTAAAGAAATGCCAGGCTCTGGAGGGTCCGGCGCGCGCCAGCGAGCAG 688
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
 DB 689 GCGCGGACCTGGAGAGTGGCGGAGGCGCTGCGAGCAGCAGCAGCAGCGTGGAGTGGAC 748
 QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
 DB 749 CAGCTGCGATGTCAGGCCAGAGCGTGGAGGCGCGCTCCGATGATGAGCGCCAGCGGCC 808
 QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
 DB 809 TCGAGGAGAAAGAGGAGCTGGCCCAAGTTGAGGTGGCTTATCACCAGCTCTTCCAGAA 868
 QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260

Db 869 TACGACACACATCAAGACGCGTGGTGGCAGTGGAGCGAGGATGAGCTG 928
 Qy 261 GluAspLeuLysGlnLeuGlnGlnAlaGluAlaLeuValAlaLysGlnGluVal 280
 Db 929 GAAGATCTCAACAGCAGCTCCAGCAGCGCCGAGGAGGCGCTGGTGGCCAAACAGGAGGTG 988
 Qy 281 IleAspLysLeuLysGlnGluAlaGlnGlnHisLysIleValMetGluThrValProVal 300
 Db 989 ATCGATAGCTGAAGGAGGAGCGGAGCAGCACAAGATTGTGATGAGACCGTTCCGGTG 1048
 Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
 Db 1049 CTGAAGCCCGAGCGGATATCTACAAGCGGACTTCCAGGCTGAGAGGCGAGCCCGGGAG 1108
 Qy 321 LysLeuAlaGluLysLysGlnLeuLeuGlnGlnGlnLeuGlnGlnLeuArgGluThr 340
 Db 1109 AAGCTGGCCGAGAGAGGAGCTCTCCAGGAGCAGCTGAGCAGCTGAGGAGGAGTAC 1168
 Qy 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaAspGlnAlaAspMetArgLysArgHis 360
 Db 1169 AGCAACTGAAGCGCAGCTGTCAAGAGTGGCCAGGATCGAGATGAGGAGCGGAT 1228
 Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLeuSerSerProLeuAla 380
 Db 1229 GTGAGGTCTCCAGGCGCCCTTGGCCCGCCCTGCTTCTCTCTCTCTCTCTCTCTGCCC 1288
 Qy 381 LeuProSerGlnArgSerProProGluLysProProAspPheCysCysProLysCys 400
 Db 1289 CTGCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1348
 Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnGlnHisValMetGluCysIleGlu 419
 Db 1349 CAGTATCAGGCGCTGTATGGACACCTTGCAGATACATGTCATGAGTGCAATTGAG 1405
 RESULT 5
 ID AAF21149 standard; DNA; 1994 BP.
 AC AAF21149;
 XX
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human low adenosine antisense oligonucleotide related sequence #2716.
 XX
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX W0200062736-A2.
 PN
 XX
 XX 26-OCT-2000.
 PD
 XX
 XX 24-MAR-2000; 2000WO-US008020.
 PF
 XX
 XX 06-APR-1999; 99US-0127958P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 PI
 XX Nyce JW;
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT

adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Disclosure; Page 1045-1046; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.8e-153 Length: 1994
 Score: 2115.00 Matches: 419
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-377-795-2 (1-419) x AAF21149 (1-1994)

Qy 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
 Db 149 ATGAATAGGCACCTCTGGAGAGCCAACTGTGTAGATGGTGCAGCCAGTGGTGGCCCG 208
 Qy 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
 Db 209 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGTCGAC 268
 Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnCysGluCysGluGluAsnGlnGlu 50
 Db 269 CTGCTTTCAACAACAGGGCGCTCTCTGAGACCCCTCAGCGCTGCTGGAGAGAGAAATCAAGAG 328
 Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
 Db 329 CTCGAGATGCCATCCGCGAGAGCAACAGATCTTCGGGAGCGCTGCGAGAGAGCTTCTG 388
 Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
 Db 389 CATTTCCAAAGCCAGCCAGGAGGAGAGAGAGTTCCTCATGTGTCAAGTTCAGAGAGGCC 448
 Qy 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
 Db 449 AGGAAGCTGTGTGAGAGACTCGGCTGGAGAGAGCTCGATCTGAAGAGGAGGAGGAGGAG 508
 Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140

Db 509 GCTCTGCGGAGGTGGAGCACCTGAAGAGATGCGCAGCAGCAGATGGCTGAGGACAAAGGCC 568
 QY 141 SerValysAlaGlnValThrSerLeuLeuGluGluSerGlnSerArgLeu 160
 Db 569 TCTGTGAAGACCCAGGTGAGCTCTTCTCGGGAGCTGCGAGAGCCAGAGTCGCTTG 628
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGluArgAlaAlaSerGluGln 180
 Db 629 GAGGTGCCACTAAGGAATGCCAGGCTCTGAGGGTCGGCGCGGCGGCAGGAGCAG 688
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGlnValAsp 200
 Db 689 GCGCGGAGCTGGAGAGTGCAGCGAGCGCTGCGAGCAGCAGCAGCAGCGTCGAGGTGGAC 748
 QY 201 GlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
 Db 749 CAGCTGCGCATGAGGCCAGAGCGTGGAGCGCGCTCCGATGGAGCGCCAGCGGCC 808
 QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
 Db 809 TCGGAGGAGAAGAGGAGCTGGCCAGCTTCAGGTGGCTTATCACCAGCTCTTCCAGAA 868
 QY 241 TyrAspHisHisLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
 Db 869 TAGCACAAACACATCAAGAGCAGCGTGTGGCAGTGCAGCGAAGCGAGCAATGCAGCTG 928
 QY 261 GluAspLeuLysGlnGlnGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
 Db 929 GAAGATCTCAACAGCAGCTCCAGCAGCGCGAGGCGCTTGTGGCCAAACAGGAGGTG 988
 QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
 Db 989 ATCGATAAGCTGAAGGAGGAGCGCAGCAGCACAGATTGTGATGGAGCCGTTCGGTG 1048
 QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
 Db 1049 CTGAAGCCCGAGCGGATATCTACAAGCGGAGCTTCCAGGCTGAGAGCGCGCGGAG 1108
 QY 321 LysLeuAlaGluLysLysGluLeuGlnGlnGluGlnLeuGlnLeuGlnArgGluTyr 340
 Db 1109 AAGCTGCCGAGAGAAGGAGCTCTCTGAGGAGCAGCTGGAGCAGCTGCAGAGGGAGTAC 1168
 QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
 Db 1169 AGCAAACTGAAGCCAGCTGTAGGAGTGCAGCAGGATCGAGCAGCATGAGAGCGGCAT 1228
 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
 Db 1229 GTCGAGGTCTCCAGGCGCCCTTGGCCCGCCCTGCTTACCTCTCTCCCTGGCC 1288
 QY 381 LeuProSerGlnArgSerProGluGluProGluProAspPheCysCysProLysCys 400
 Db 1289 CTGCCAGCAGAGGAGGAGCCCGCCGAGGAGCCACTTCTGCTGTCCAAAGTGC 1348
 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
 Db 1349 CAGTATCAGSCCCCTGATATGGACACCTCTCAGATACATCTCATGGAGTCATTGAG 1405

RESULT 6
 ADA44705
 ID ADA44705 standard; DNA; 1994 BP.
 XX AC
 AC ADA44705;
 XX
 DT 20-NOV-2003 (first entry)
 DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 3.
 DE
 XX Antisense oligonucleotide; cytostatic; immunosuppressive;
 KW antiinflammatory; gene therapy; hyperproliferative disorder; cancer;
 KW autoimmune; inflammatory disorder; inhibitor-kappa B kinase-gamma; gene;
 KW db.
 XX

OS Homo sapiens.
 XX WO2003031576-A2.
 XX PD 17-APR-2003.
 XX 03-OCT-2002; 2002WO-US031809.
 XX 06-OCT-2001; 2001US-00972607.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Wyatt JR;
 XX WPI; 2003-457242/43.
 XX
 PT New compound having sequence targeted to nucleic acid encoding inhibitor-
 PT kappa B kinase-gamma, useful for preparing composition for treating e.g.,
 PT cancer, or inflammatory or autoimmune disorder.
 XX
 PS Example 15; Page 82-85; 106pp; English.
 XX
 CC The invention relates to an antisense compound that is targeted to a
 CC nucleic acid encoding inhibitor-kappa B kinase-gamma, specifically
 CC hybridizing to the nucleic acid encoding inhibitor-kappa B kinase-gamma
 CC and inhibiting its expression. Compounds of the invention are antisense
 CC oligonucleotides comprising at least one modified internucleoside
 CC linkage, which is a phosphorothioate linkage, at least one modified sugar
 CC moiety, which is a 2'-O-methoxyethyl sugar moiety, or at least one
 CC modified nucleobase, which is a 5-methylcytosine. Preferably, the
 CC antisense oligonucleotide is a chimeric oligonucleotide. The compound of
 CC the invention is useful for preparing a composition for treating a
 CC hyperproliferative disorder e.g., cancer, or an autoimmune or
 CC inflammatory disorder. The methods are useful for inhibiting the
 CC expression of inhibitor-kappa B kinase-gamma in cells or tissues, and
 CC treating an animal having a disease or condition associated with
 CC inhibitor-kappa B kinase-gamma. The current sequence represents the human
 CC inhibitor-kappa B kinase-gamma encoding sequence that was used to design
 CC the antisense oligonucleotides of the invention.
 XX
 SQ Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 8 8e-153 Length: 1994
 Score: 2115.00 Matches: 419
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-377-795-2 (1-419) x ADA44705 (1-1994)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
 Db 149 ATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGTCAGCCAGTGGTGGCCG 208
 QY 21 AlaAlaAspGlnAspValLeuGluGluSerProLeuGlyLysProAlaMetLeuHis 40
 Db 209 GCAGCAGATCAGACGCTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 268
 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60
 Db 269 CTGCTTTCAGACAGGGCGCTCTGTAGACCTCCAGCGCTGCTGGAGGAGATCAAGAG 328
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeu 80
 Db 329 CTCGAGATGCCATCCGCGAGACCAACAGATTCTCGGAGCGCTGCGAGGAGCTCTG 388
 QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
 Db 389 CATTTCCAAAGCCAGCCAGAGGAGGAGAGGAGTTCCTCATGTGCAAGTTCCAGGAGGCC 448
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120

Db 449 AGGAACTGCTGGAGAGACTCGCGCTGGAGAGACTGATCTGAAGAGGCGAGAGAGCGAG 508
Qy 121 AlalaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
Db 509 GCTCTGCGGAGGTGGAGCACCTGAAGAGATGCGAGCAGCAGATGCTGAGGACAGGCGC 568
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
Db 569 TCTGTGAAGCCCAAGGTGAGCTCTTGTCTGGGAGCTCGAGAGAGCCAGAGTGCCTTG 628
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 629 GAGCTGCCACTAAGGAATGCCAGGCTCTGGAGGTCGGGCCCGGCCAGCGAGCGAG 688
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
Db 689 GCGCGCAGCTGGAGAGTGAAGCGAGCGAGCGCGCTGCGAGCAGCACAGCGTGCAGGTGGAC 748
Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 749 CAGCTGCGCATGAGGCGCCAGAGCGGTGGAGCGCGCTCGCATGGAGCGCCAGCGCGCC 808
Qy 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
Db 809 TCGAGGAGAGAGAGAGCTGGCCAGTTGCGAGTGGCTATCACCAGCTCTTCCAGAA 868
Qy 241 TyrAspHisHisLysSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 869 TAGCACACACATCAAGAGCAGCGTGGTGGCAGTGCAGCGGAAGCGAGGAATGCAGCTG 928
Qy 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 929 GAAGATCTCAACAGCAGCTCCAGCAGCGCGAGGCGCTGCTGGTGCCTCAACAGAGGTG 988
Qy 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db .989 ATCGATAAGCTGAAGAGGAGCGCGAGCAGCACAGATTGTGATGGAGACCGTTCGGGTG 1048
Qy 301 LeuLysAlaGlnAlaAspLysLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 1049 CTGAGGCGCCAGCGGATATCTACAAGCGGACTTCCAGGCTGAGAGCGAGCGCGGAG 1108
Qy 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnArgGluTyr 340
Db 1109 AAGTGGCCGAGAGAGAGGCTCTCTGAGGAGCAGCTGGAGCAGCTGCAGAGGAGTAC 1168
Qy 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgLleGluAspMetArgLysArgHis 360
Db 1169 AGCAAACTGAAGCCAGCTGTGAGGAGTCCGCGAGATCGAGGACATGAGGAAGCGGCAT 1228
Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 1229 GTGAGGTCTCCAGGCGCCCTTGCCTCCCGCGCCCTGCTCTCTCTCTCTCTCTCTCT 1288
Qy 381 LeuProSerGlnArgSerProGluGluProProAspPheCysCysProLysCys 400
Db 1289 CTGCCCCAGCAGAGGAGGAGGCCCCCGGAGGAGCCACCTGACTTCTGTGTCTCCAGTGC 1348
Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 1349 CAGTATCAGGCGCCCTGATATGGACACCTCTGAGATACATGTCTATGGATGTCATTGAG 1405

RESULT 7

ABZ96843
ID ABZ96843 standard; DNA; 1994 BP.
XX
AC ABZ96843;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human nucleic acid sequence.
XX

Qy 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 149 ATGAATAGGCACCTCTGGAAGAGCAACTGTGTGAGATGTTGTCAGCCAGTGGTGGCCG 208
Qy 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 209 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTTGGGGAAGCCAGCATGCTGCAC 268
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60

Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
Miller S, Tang L, Shahabuddin S;

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired
respiration, has oligo(s) antisense to specific gene(s) or its
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
ubiquinone.

Disclosure; SEQ ID NO 12085; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a
first active agent comprising an oligonucleotide antisense to the
initiation codon, coding region, 5' or 3' end genomic flanking regions,
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
junctions of genes encoding a polypeptide associated with lung and/or
nasal airway dysfunction and a second active agent comprising an
antiinflammatory steroid and ubiquinone. A composition of the invention
has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
immunosuppressive, and cytostatic activity. The composition may have a
use in antisense gene therapy. The composition is useful for treating or
preventing a respiratory, lung or malignant disease or condition, also
for enhancing the prophylactic or therapeutic respiratory effect of an
antiinflammatory steroid in a subject, for reducing or depleting levels
of, or reducing sensitivity to adenosine, reducing levels of adenosine
receptor, producing bronchodilation, increasing levels of ubiquinone or
lung surfactant in a subject's tissue, or treating bronchoconstriction,
lung inflammation, lung allergies, or a respiratory disease or condition.
Note: The sequence data for this patent is not represented in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.8e-153	Length:	1994
Score:	2115.00	Matches:	419
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-377-795-2 (1-419) x ABZ96843 (1-1994)

Db 269 CTGCTTTCAAGACAGGCGCTCTCTGAGACCTCTCAGCGCTGCTGGAGGAGATCAAGAG 328
QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
Db 329 CTCGAGATGCCATCCGCGAGAGCAACAGATTCTGCGGAGCGCTCGAGGAGCTTCTG 388
QY 81 HisPheGlnAlaSerGlnArgGluGluPheLeuMetCysLysPheGlnGluAla 100
Db 389 CATTTCCAGCCAGCCAGAGGAGGAGAGAGTTCTCTCATGTGCAAGTTCAGGAGGCC 448
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 449 AGGAAACTGTGTGGAGAGACTCGGCTCGAGAAGCTCGATCTGAAGAGCGCAGAGGACG 508
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
Db 509 GCTCTGGGGAGGTGGAGCACTGGAAGATGCCAGCAGAGATGGCTGAGGACAAGGCC 568
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
Db 569 TCTGTGAAGCCCAAGGTGACGTCTTCTGCGGAGGCTGCAGAGCCAGACAGTTCGCTTG 628
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 629 GAGGCTGCCACTAAGGAATGCCAGGCTCTGAGGGTCCGGCCGGCGCCAGCGAGCAG 688
QY 181 AlaArgGlnLeuGlnSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
Db 689 GCGCGGAGCTGAGAGTGGCGGAGCGCTGCGAGCAGCAGCAGCAGCTGCGAGGTGGAC 748
QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaLeuArgMetGluArgGlnAlaAla 220
Db 749 CAGCTGCGCATGCGAGGCCAGAGCGTGGAGCGCGCTCCGCATGGAGCGCCAGCGGCC 808
QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
Db 809 TCGGAGGAGAAGAGGAGCTGGCCAGTTGTCAGTGGCTTATCACAGCTCTTCCAAGAA 868
QY 241 TyrAspAsnHisIleLysSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 869 TAGCAACACACATCAAGAGCAGCGTGGTGGCAGTGAGCGGAAGCGAGGAATGCACTG 928
QY 261 GluAspLysLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 929 GAAGATCTCAACAGCAGCTCCAGCAGCCCGAGAGGCCCTGTGTGCCAACAACAGGAGTG 988
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db 989 ATCGATAAGCTGAAGGAGGAGCGCAGCAGCAAGATTGTGATGGAGACCGTTCCGGTG 1048
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 1049 CTGAAGGCCCGAGCGGATATCTCAAGCGCGATCTCCAGGCTGAGAGGCGCCGGGAG 1108
QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnLeuGlnLeuGlnArgGluTyr 340
Db 1109 AAGCTGGCCGAGAAGAGAGCTCTCTGAGAGCAGCTGGAGCAGCTGCAGAGGGAGTAC 1168
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
Db 1169 AGCAAACTGAAGGCCAGCTGTGAGGAGTCCGCCAGGATCCAGGACATGAGGAAGCGCAT 1228
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 1229 GTCCAGGTCTCCAGGCGCCCTTTGCCCGCCCGCCCTGCTACCTCTCTCTCCCTGGCC 1288
QY 381 LeuProSerGlnArgSerProGluGluProProAspPheCysCysProLysCys 400
Db 1289 CTGCCAGCCAGAGGAGGAGCCCCCGAGGAGCCACCTGACTTCTGTGTCCCAAGTGC 1348
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419

Db 1349 CAGTATCAGGCCCTGTATGGACACCCTGCAGATCATGTGATGGAGTGCATTGAG 1405
RESULT 8
ABV75393
ID ABV75393 standard; DNA; 1994 BP.
XX AC ABV75393;
XX 18-MAR-2003 (first entry)
DT Human NEMO polypeptide encoding DNA.
XX
DE CD40; NF-kappaB essential modulator; NEMO; CYLD; immunosuppressive;
XX antiinflammatory; cytostatic; gene therapy; human; gene; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
CDS 149..1408
FT /*tag= a
FT /product= "NEMO"
XX
PN WO200292761-A2.
XX 21-NOV-2002.
XX 07-MAY-2002; 2002WO-US014570.
XX 08-MAY-2001; 2001US-00851673.
XX (IMMV) IMMUNEX CORP.
XX Derry JMJ, Fanslow WC, Dougall WC;
PI WPI; 2003-120669/11.
DR P-PSDB; ABB82782.
XX
PT Identifying compounds that alter one or more biological activities of
PT CD40 by modulating the binding of NEMO and CYLD, useful for treating
PT disorders of the immune system, and inflammatory and cancer diseases.
XX Example 5; Page 33-35; 48pp; English.
XX The invention relates to methods of identifying compounds that alter one/
XX more biological activities of CD40. One method involves screening for
XX molecules that modulate the binding of NF-kappaB essential modulator
XX (NEMO) and CYLD. The methods and compositions of the invention of
XX determining compounds that agonize or antagonize a CD40 signaling
XX activity, are useful for the further definition of CD40-mediated
XX signaling pathways, and for manipulation of CD40-mediated cellular
XX responses. They also provide therapeutic agents for treating disorders of
XX the immune system, and inflammatory and cancer diseases. The present
XX sequence represents a DNA encoding the human NEMO polypeptide
SQ Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 8.8e-153 Length: 1994
Score: 2115.00 Matches: 419
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-377-795-2 (1-419) x ABV75393 (1-1994)
QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 149 ATGATAGACCACTCTGGAGAGGCCAACTGTGTGAGATGGTGAGCCCGAGTGTGGCCCG 208
QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 209 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGGAAGCCAGCATGCTGCAC 268

CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX SQ Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.9e-153 Length: 1994
 Score: 2115.00 Matches: 419
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-377-795-2 (1-419) x ABD20692 (1-1994)

QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
 Db 149 ATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGTCAGCCCACTGGTGGCCCG 208
 QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysPheAlaMetLeuHis 40
 Db 209 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGAAGCCAGCCATGCTGCAC 268
 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
 Db 269 CTGCTTCAGAACAGGGCGCTCTGAGACCCCTCCAGCGCTGCTGGAGGAGATCAAGAG 328
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
 Db 329 CTCGAGATGCCATCCGGCAGAGCAACAGATTCTCGGAGCGCTGCGAGGAGCTTCTG 388
 QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
 Db 389 CATTTCCAGCCAGCCAGAGGAGGAGAGAGTCTCTCATGTGCAAGTTCCAGAGAGGCC 448
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
 Db 449 AGCAAACTGTGTGAGAGACTCGCGCTGGAGAGCTCGATCTGAAGAGGACAGAGGAGCAG 508
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
 Db 509 GCTCTCGGAGGTGGAGCACCTGAAAGAGATGCCAGCAGCAGATGCTGAGGACAAAGGCC 568
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerArgLeu 160
 Db 569 TCTGTGAAAGCCAGGTGAGTCTCTTGTCTGGGGAGCTGCGAGAGCCAGAGTCTGCTTG 628
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
 Db 629 GAGGCTGCCACTAAGGATGCCAGGCTCTGGAGGGTTCGGGCCCGGGCCAGCAGCAG 688
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
 Db 689 GCCTGCGCAGCTGAGAGTGAAGCGGAGGCGCTGAGCAGCAGCACAGCGTGCAGGTGGAC 748
 QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
 Db 749 CAGCTCGCATGTCAGGCGCAGAGCGTGGAGGCGCGCTCCGATGAGCGCCAGCGGCC 808
 QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
 Db 809 TCGGAGAGAGAGAGAGCTGGCCCACTGTGAGTGGCGCTATCACCAGCTCTTCCAGAA 868
 QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
 Db 869 TACGCAACACCATCAAGAGCAGCGTGTGGCAGTGAGCGGAAGCGAGGAATGCAGCTG 928
 QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValLysGlnGluVal 280
 Db 929 GAAGATCTCAAAAGCAGAGCTCCAGCAGGCGGAGGAGGCCCTGTGTGCCAAACAGAGGAG 988

QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
 Db 989 ATCGATAAGCTGAAGGAGGAGGCGGAGCAGCACAAAGATTGTGTGAGGACCGTTCGGGTG 1048
 QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
 Db 1049 CTGAAGGCCCGAGCGGATATCTACAAGGCGGACTTCCAGGCTGAGAGCGCGCGGAG 1108
 QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnLeuGlnLeuGlnLeuGlnArgGluTyr 340
 Db 1109 AAGCTGGCCGAGAAGAGGAGCTCTTCAGAGCAGCTGGAGCAGCTGCGAGGAGGATAC 1168
 QY 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
 Db 1169 AGCAAACTGAAGGCCAGCTGTCAAGAGTCGCCAGGATCGGACGATGAGAGCGGCAT 1228
 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
 Db 1229 GTCGAGGCTCTCCAGGCGCCCTTGGCCCCCGCCCTGCTTCTCTCTCCCTGGCC 1288
 QY 381 LeuProSerGlnArgSerProGluGluProProAspPheCysCysProLysCys 400
 Db 1289 CTCCCGAGCCAGAGGAGGAGCCCCCGGAGGAGCCACTTCTGCTGTCCCAAGTGC 1348
 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
 Db 1349 CAGTATCAGGCCCTGATATGAGACCCCTGCAGATACATGTCATGAGTGCATTGAG 1405

RESULT 10

AAZ07513
 ID AAZ07513 standard; DNA; 2009 BP.

XX AAZ07513;

DT 26-NOV-1999 (first entry)

DE Human RIP-associated protein (RAP-2) encoding DNA.

KW Receptor interacting protein; RIP-associated protein-2; RAP-2; RIP;
 KW inflammation; cell death; cell survival; septic shock; hepatitis;
 KW graft versus host rejection; diabetes; multiple sclerosis; tumor;
 KW HIV infection; p55-receptor; FAS-receptor; human; ss.

XX Homo sapiens.

XX WO9947672-A1.

XX 23-SEP-1999.

XX 18-MAR-1999; 99WO-IL000158.

XX 19-MAR-1998; 98IL-00123758.

XX 01-SEP-1998; 98IL-00126024.

XX (VEDA) YEDA RES & DEV CO LTD.

PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.

XX Wallach D, Kovalenko A, Horwitz MS, Li Y;

XX WPI; 1999-562113/47.

DR P-PSDB; AAV27430.

PT New receptor interacting protein-associated protein-2, used to develop
 PT products for treating, e.g. septic shock, tumors or HIV infection.

XX Claim 4; Fig 1A-B; 132pp; English.

CC This DNA encodes a receptor interacting protein (RIP)-associated protein
 CC -2 (RAP-2). The RAP-2 proteins, isoforms, analogs, fragments or
 CC derivatives or DNA can be used for the modulation or mediation of the RIP
 CC modulated/mediated intracellular effects on the inflammation, cell death
 CC or cell survival pathways in which RIP is involved directly, or
 CC indirectly via other modulators/mediators of these pathways. They can be

CC used for treating e.g. septic shock, graft versus host rejection, acute
 CC hepatitis, diabetes or multiple sclerosis. They can also be used for
 CC treating tumor cells or HIV-infected cells or other diseased cells. The
 CC RAP-2 binding proteins can be used for modulating/mediating the function
 CC of RAP-2. The products can also be used for diagnostic purposes, e.g. for
 CC identifying disorders related to abnormal functioning of cellular effects
 CC mediated by the p55-R, FAS-R or other related receptors

XX Sequence 2009 BP; 418 A; 587 C; 643 G; 356 T; 0 U; 5 Other;

Alignment Scores:

Pred. No.: 8.87e-153 Length: 2009
 Score: 2115.00 Matches: 419
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-377-795-2 (1-419) x AAZ07513 (1-2009)

QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
 DB 154 ATGAATAGGACCTCTGGAAAGACCAACTGTGTGAGATGTCAGCCCAAGTGTGTCGCCG 213
 QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
 DB 214 GCAGCAGTACAGACGTACTGGCGGAGAGTCTCTCTGGGAAGCCACCATGCTGCAC 273
 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60
 DB 274 CTGCTTCAGAACAGGCGCTCTGAGACCTCCAGCGCTGCTGGAGAGAAATCAAGAG 333
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80
 DB 334 CTCGAGATGCCATCCGGCAGAGCAACACAGATTCTCGGGAGCGCTGCGAGAGCTTCTG 393
 QY 81 HisPheGlnAlaSerGlnArgGluGlyLysGluPheLeuMetCysLysPheGlnGluAla 100
 DB 394 CATTTCCAAAGCCAGCAGAGGAGGAGAGGAGTTCTCTATGTGCAAGTTCAGAGAGGCC 453
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGlyLysLeuAspLeuLysArgGlnLysGluGln 120
 DB 454 AGAAATCTGTGGAGAGACTCGGCTCTGGAGAGCTGATCTCAAGAGGAGAGAGAGCAG 513
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaCysLysAla 140
 DB 514 GCTCTGGGAGGTGGAGACCTGAAGATGCCAGACAGATGGCTGAGAGACAGGCC 573
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
 DB 574 TCTGTGAAGCCAGGTGACGCTCTTGTCTGGGGAGCTGCAGAGAGCCAGAGTCGCTTG 633
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaAlaSerGluGln 180
 DB 634 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGGCCCGGCGCCAGCAGCAG 693
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGlnValAsp 200
 DB 694 GCCGGCAGCTGGAGAGTARGCGCGAGGCGCTGCAGAGCAGCAGCGTGCAGGTGGAC 753
 QY 201 GlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
 DB 754 CAGCTCGCATGTCAGGGCCAGAGCGTGGAGGCGCGCTCCGTCATGGAGCGCCAGCGCC 813
 QY 221 SerGluGlyLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
 DB 814 TCGAGAGAGAGAGAGAGTGGCCAGTTCAGAGTGGCTATCACAGCTCTTCCAGAA 873
 QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
 DB 874 TAGCAACAACACATCAAGAGCAGCGTGTGGCAGTGGAGCGGAGCGAGGAGTGCAGCTG 933
 QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280

DB 934 GAAGATCTCAAAACAGCAGCTCCAGCAGGCGGAGGAGCCCTGGTGCCTCAACAGAGGTTG 993
 QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGlnThrValProVal 300
 DB 994 ATCGATAAGCTGAAGAGAGGAGCCGAGCAGCAAGATTGTATGGAGACCGTTCCGGTG 1053
 QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
 DB 1054 CTGAAGGCCCGAGCGGATATCTACAAGCGGACTTCCAGGCTGAGAGGCGAGCCCGGAG 1113
 QY 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnLeuGlnGlnLeuGlnArgGluTyr 340
 DB 1114 AAGTGGCCGAGAAAGAGAGCTCTTCAGGAGCAGCTGAGCAGCTGCAGAGGAGTAC 1173
 QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
 DB 1174 AGCAACTGAAGGCCAGCTGTGAGAGTGGCCAGATCGAGACATGAGGAGCGGCAT 1233
 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
 DB 1234 GTCGAGGTCTCCAGGCCCTTGCCCCCGCCCTGCTACCTCTCTCTCTCTCTCTCTCT 1293
 QY 381 LeuProSerGlnArgArgSerProProGluGluProProAspPheCysCysProLysCys 400
 DB 1294 CTGCCAGCCAGAGAGAGGCCCGCCCGAGGAGCCACCTGACTTCTGTGTCTCCCAAGTC 1353
 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
 DB 1354 CAGTATCAGGCCCTGATATGGACACCTTCAGATACATGTCATGAGTGCATTGAG 1410
 RESULT 11.
 ACD23012
 ID ACD23012 standard; cDNA; 2035 BP.
 XX
 AC ACD23012;
 DT 25-AUG-2003 (first entry)
 XX
 DE Human NEMO cDNA.
 KW Human; gene; ss; NF-kappaB essential modulator; nuclear factor kappa B;
 KW incontinentia pigmenti; X-linked disorder; chromosome Xq28; NEMO;
 KW immunomodulatory; dermatological; osteopathic; neuropathic;
 KW apoptosis-related disease; immune-system related disease;
 KW blood vessel-related disease; skin defect; dental defect; osteopetrosis;
 KW ophthalmologic defect; neurological defect.
 XX Homo sapiens.
 OS
 XX
 XX US2003032055-A1.
 XX
 PD 13-FEB-2003.
 XX
 XX 22-MAY-2001; 2001US-00863049.
 XX
 XX 22-MAY-2000; 2000US-0206223P.
 XX
 XX (KENW/) KENNRICK S J.
 PA (WOFF/) WOFFENDIN H.
 PA (MUNN/) MUNNICH A.
 PA (SWAH/) SMAHI A.
 PA (ISRA/) ISRAEL A.
 PA (POUS/) POUSTKA A.
 PA (HEIS/) HEISS N.
 PA (DURS/) D'URSO M.
 PA (LEWI/) LEWIS R A.
 PA (NELS/) NELSON D L.
 PA (ARAD/) ARADHYA S.
 PA (LEVY/) LEVY M.
 XX
 PI Kenrick SJ, Woffendin H, Munnich A, Smahi A, Israel A;
 PI Poustka A, Heiss N, D'urso M, Lewis RA, Nelson DL, Aradhy S;

PI Levy M;
 XX WPI: 2003-492063/46.
 DR P-PSDB; ABO17485.
 XX
 PT Detection of necrosis factor-kappa B related medical condition in
 PT organism, by obtaining sample from the organism, and analyzing the sample
 PT for alteration in specified amino acid sequences.
 XX
 XX Disclosure; Page: 44pp; English.
 XX
 CC The invention relates to a nuclear factor-kappa B (NF-kappa B) related
 CC medical condition in an organism being detected by obtaining a sample
 CC from the organism, and analyzing the sample for an alteration in a the
 CC nuclear factor kappaB essential modifier (NEMO) gene or protein sequence
 CC (neither shown in the specification). The alteration results in
 CC inactivation of NF-kappa B. Also included are treating or preventing NF-
 CC kappa B related medical condition in an organism by administering the
 CC NEMO protein to the organism and screening a test organism for a compound
 CC for the treatment of NF-kappa B related medical condition (by
 CC administering the compound to the organism, and assaying for an
 CC improvement in the NF-kappa B related medical condition). The method
 CC useful is for detecting NF-kappa B related condition, e.g. incontinentia
 CC pigmenti (IP), apoptosis-related disease, immune-system related disease,
 CC blood vessel-related disease, skin defect, dental defect, osteopetrosis,
 CC ophthalmologic defect, or neurologic defect, in an organism, i.e. human
 CC including affected individual, carrier individual, or noncarrier
 CC individual. The NEMO gene is located on chromosome Xq28, incontinentia
 CC pigmenti being an X-linked disorder. Experiments in this study show
 CC variations in exon 2, 10, 9 and particularly intron 3 to be linked to
 CC familial incontinentia pigmenti. The present sequence is the human NEMO
 CC cDNA. Note: The present sequence is not shown in the specification but
 CC was obtained from Genbank using the reference number given in the
 CC specification
 XX
 SQ Sequence 2035 BP; 425 A; 592 C; 637 G; 381 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9, 01e-153 Length: 2035
 Score: 2115.00 Matches: 419
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-377-795-2 (1-419) x ACD23012 (1-2035)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
 DB 186 ATGAATAGGCACCTCTGGAAGAGACCAACTGTGTGAGATGGTGCGAGCCCGAGTGTGCGCCG 245
 QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
 DB 246 GCAGCAGATCAGACGCTACTGGCGGAAGAGTCTCTCTGCGGGAAGCAGCCATGCTGCAC 305
 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
 DB 306 CTGCCTTCAGAACAGGGCGCTCTTGAGACCTCCAGCGCTGCTGAGGAGGAGTCAAGAG 365
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
 DB 366 CTCGAGATGCCATCCGGCAGAGCAACAGATTCTCGCGGAGCGCTGCGAGGAGCTTCG 425
 QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
 DB 426 CATTTCCAGCCAGCCAGAGGGAGGAGAGGAGTCTCTATGTCGAAGTTCCAGGAGGCG 485
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
 DB 486 AGGAACCTGTGTGAGAGACTCGGCCCTGGAGAACCTCGATCTGAAGAGGCGAAGAGGACG 545
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140

DB 546 GCTCTCGCGAGGTGGAGCACCTGAAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 605
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
 DB 606 TCTGTGAAAGGCCAGGTGAGCTCTTGTCTCGGGAGGCTGCGAGGAGACCGAGAGTCGCTTG 665
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
 DB 666 GAGGCTGCCACTAAGGANTGCCAGGCTCTGGAGGGTCGGGCCCGGGCGGCGAGGACAG 725
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
 DB 726 GCGCGCGAGCTGGAGAGTGAGCGGAGGCGCTGCGAGCAGCAGCAGCAGCTGCGAGTGGAC 785
 QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
 DB 786 CAGCTCGCATGCGAGGCCAGAGCGTGGAGGCGCGCTCCGATGGAGCGCCAGGCGGCC 845
 QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
 DB 846 TCGGAGGAGNAGNAGAGTGGCCAGTTCAGGTGGCTTATCACCAGCTTCTTCCAAGAA 905
 QY 241 TyrAspAsnHisLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
 DB 906 TACGACAAACCATCAAGAGCAGCGTGGTGGGCAGTGAGCGGAAGCAGGAATGCAGCTG 965
 QY 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
 DB 966 GAAGATCTTCAACAGCAGCTCCAGCAGGCGGAGGCGCTGCTGTCGCAACAGGAGGTG 1025
 QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysLysValMetGluThrValProVal 300
 DB 1026 ATCGATACTGAGGAGGAGGCGGCGGAGCAGCAGCAAGATTGTGATGAGACCTGTCGGTG 1085
 QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
 DB 1086 CTGAAGGCCAGCGGATATCTACAAGCGGAGCTTCAGGCTGAGAGGCGGCGCGGAG 1145
 QY 321 LysLeuAlaGluLysGluLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGluTyr 340
 DB 1146 AAGCTGGCGGAGAAAGAGAGTCTCTGCGAGGAGCAGCTGGAGCAGCTGCGAGGAGTAC 1205
 QY 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
 DB 1206 AGCAACTGAGGCCAGCTGTGAGGAGTGGCCAGGATCGAGGACATGAGGAAGCGCAT 1265
 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLeuSerSerProLeuAla 380
 DB 1266 GTCGAGGTCTCCAGGCGCCCTTGGCCCGCCCTGCTTACCTCTCTCTCCCTGGCC 1325
 QY 381 LeuProSerGlnArgSerProGluGluProGluProAspPheCysCysProLysCys 400
 DB 1326 CTGCCAGCAGAGGAGGAGGCGCCCGGAGGAGCCACCTGACTTCTGCTGTCTCCCAAGTC 1385
 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
 DB 1386 CAGTATCAGGCCCTGATATGACACCTTCAGATACATGTGATGAGTGCAATTGAG 1442

RESULT 12
 AAA35028
 ID AAA35028 standard; DNA; 8631 BP.
 XX
 AC AAA35028;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2717.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.
 XX Homo sapiens.
 OS WO200009525-A2.
 PN 24-FEB-2000.
 PD 03-AUG-1999; 99WO-05017712.
 XX 03-AUG-1998; 98US-0095212P.
 PR (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 PI WPI; 2000-205971/18.
 DR
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 XX Disclosure; Page 969-971; 1343pp; English.
 PS
 XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA3213 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO.: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 8631 BP; 2280 A; 2050 C; 2270 G; 2031 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4,95e-152 Length: 8631
 Score: 2115.00 Matches: 419
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-09-377-795-2 (1-419) x AAA35028 (1-8631)
 QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
 DB 6786 ATGAAATAGGACCTCTGGAAAGAGCAACTGTGTGATGGTGCAGCCAGGTGGTGGCCG 6845
 QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
 DB 6846 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAGGACGACCATGCTGCAC 6905

QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
 DB 6906 CTGCCTTCAGAACACAGGGCGCTCCTGAGACCCCTCCAGCGCTGCCTGAGGAGAATCAAGAG 6965
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeu 80
 DB 6966 CTCGAGATGCCATCCCGCAGAGCAACACAGATTCTGCGGAGCGCTGCGAGAGGCTTCTG 7025
 QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
 DB 7026 CATTTCCAGCCAGCCAGAGGAGGAGAGAGATTCTCATGTGCAAGTTCCAGGAGGCC 7085
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGlyLysLeuAspLeuLysArgGlnLysGluGln 120
 DB 7086 AGGAAACTGTGTGAGAGACTCGGCCTGGAGAAGCTCGATCTGAAGAGGCAGAGGAGCAG 7145
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
 DB 7146 GCTCTGCGGGAGGTGGAGCACCTGAAGAGATGCCAGAGCAGATGGCTGAGGACAGGCC 7205
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
 DB 7206 TCTGTGAAAGCCAGGTGACGTCTTCTCGGGAGCTGCAGGAGAGCCAGAGTGCCTTG 7265
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
 DB 7266 GAGCTCCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGGCCCGGCGCCAGCGAGCAG 7325
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
 DB 7326 GCGCGGAGCTGGAGAGTGAGCGCGAGCGCTGCAGCAGCAGCAGCAGCTGCAGGTGGAC 7385
 QY 201 GlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
 DB 7386 CAGCTGCGCATTCAGGGCCAGAGCTGGAGCGCGCTCCGCATGTGAGCGCCAGCGCCGCC 7445
 QY 221 SerGluLysArgLysLeuAlaGlnLeuValAlaThrHisGlnLeuPheGlnGlu 240
 DB 7446 TCGAGAGAGAGAGAGAGCTGGCCCACTGTGAGGTGGCCTATCACCACTCTTCCAGAA 7505
 QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
 DB 7506 TACGACAAACACATCAAGAGCAGCGTGTGGCAGTGTGAGCGAAGCGAGGATGCAGCTG 7565
 QY 261 GluAspLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
 DB 7566 GAAGATCTCAACAGCAGCTCCAGCAGCGCGAGGAGCGCTGTGGTGGCCAAACAGAGGTG 7625
 QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
 DB 7626 ATCGATNAGCTGAAGAGGAGGCGGAGGCGAGCAGCACAAGATTGTGTGGAGACCGTTC 7685
 QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
 DB 7686 CTGAAGCCCGAGCGGATATCTCAAGCGGACTTCCAGGCTGAGAGCGAGCGCCCGGAG 7745
 QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnLeuGlnArgGluTyr 340
 DB 7746 AAGCTGCGCGAGAGAGAGGAGCTCTCTGAGAGCAGCTGAGAGCAGCTGCGAGGAGGTAC 7805
 QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
 DB 7806 AGCAAACTGAAGCCAGCTCTCAGAGGTTCGCCAGGATCGAGGACATGAGGAGCGGCAT 7865
 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
 DB 7866 GTCAGGTCTCCAGGCGCCCTTGGCCCGCCCTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 7925
 QY 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400
 DB 7926 CTCGCCAGCAG 7985
 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419

Db 7626 ATCGATAGCTGAAGGAGGAGCGCGAGCAGACAAAGATTGTGATGAGACCGTTCGGGTG 7685
 QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
 Db 7686 CTGAAGGCGCCAGGCGGATATCTCAAGGCGACTTCCAGGCTGAGAGGCGAGCCCGGAG 7745
 QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGluGlnLeuGlnLeuGlnArgGluTyr 340
 Db 7746 AAGTGGCCGAGAGAGAGGAGCTCTGTCAGAGCAGCTGAGCAGCTGAGAGGAGTAC 7805
 QY 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
 Db 7806 AGCAACTGAAGGCCACTGTGAGAGTGGCCGAGATCGAGACATGAGGAGCGCAT 7865
 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
 Db 7866 GTCGAGGTCTCCAGGCGCCCTTGGCCCGCCCTGCTACCTCTCTCTCCCTGGCC 7925
 QY 381 LeuProSerGlnArgArgSerProGluGluProGluProAspPheCysCysProLysCys 400
 Db 7926 CTGCCAGCAGAGAGAGGAGCCCGCCGAGAGGCCACTTCTGCTGCTCCCAAGTGC 7985
 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
 Db 7986 CAGTATCAGGCCCTGATATGGACACCTCGACATACATGTCTATGGATGCTTGG 8042

RESULT 14

ABZ96844
 ID ABZ96844 standard; DNA; 8631 BP.
 XX AC ABZ96844;
 XX DT 17-OCT-2003 (first entry)
 XX DE Human nucleic acid sequence.
 XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX OS Homo sapiens.
 XX FN WO200285308-A2.
 XX PD 31-OCT-2002.
 XX PF 23-APR-2002; 2002WO-US013135.
 XX PR 24-APR-2001; 2001US-0286137P.
 XX PA (EPIG-) EPIGENESIS PHARM INC.
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 XX PI Miller S, Tang L, Shahabuddin S;
 XX DR WPI; 2003-229219/22.
 XX FT Pharmaceutical composition for treating ailments associated with impaired
 FT respiration, has oligo(s) antisense to specific gene(s) or its
 FT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 FT ubiquinone.
 XX PS Disclosure; SEQ ID NO 12086; 872pp; English.
 XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive, a
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in anisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 8631 BP; 2280 A; 2050 C; 2270 G; 2031 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4.95e-152 Length: 8631
 Score: 2115.00 Matches: 419
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-377-795-2 (1-419) x ABZ96844 (1-8631)
 QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
 Db 6786 ATGATAGGACCTCTGGAGAGCAACTGTGTAGATGTGTGAGCCCGGTGGTGGCCG 6845
 QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
 Db 6846 GCAGCAGATCAGGACGTACTTGGCGAAGAGTCTCTCTGGGAAAGCCAGCATGCTGCAC 6905
 QY 41 LeuProSerGlnGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
 Db 6906 CTGCTTTTCAAGAACAGGCGCTCTCTGAGACCTTCCAGCGCTCCCTGGAGGAGAAATCAAGAG 6965
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
 Db 6966 CTCGAGATGCCATCCGCGCAGAGCAACAGATCTCTGGGAGCGCTGCGAGAGCTTCTG 7025
 QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
 Db 7026 CATTTCCAGCCAGCCAGAGGAGGAGAGAGAGTCTCTCATGTGCAAGTTCCAGAGGCC 7085
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
 Db 7086 AGGAACTGTGTGAGAGACTTGGCTGGAGAGAGCTCTGTAAGAGCCAGAGAGGAGCAG 7145
 QY 121 AlaLeuArgGluValGluHisLeuLysLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
 Db 7146 GCTCTGCGGAGGTGGAGCACCCTGAAGAGATGCCAGCAGCAGATGGCTGAGCAAGGCC 7205
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGluLeuGlnGlnSerArgLeu 160
 Db 7206 TCTGTGAAGCCAGGTGAGCTTCTGTCTGGGAGCTGCGAGAGAGCCAGAGTCTGCTT 7265
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
 Db 7266 GAGGCTGCCACTAAGGATGCTCCAGGCTCTGGAGGTCTGGCGCCGGCGGCGGAGCAG 7325
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValasp 200
 Db 7326 GCGCGGAGCTGGAGAGTGGAGCGCGGCTGCGAGCAGCAGCAGCAGTGTGAGTGTGAC 7385
 QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGlnArgGlnAlaAla 220
 Db 7386 CAGCTGCGCATGAGGCGCCAGCGCTGGAGCGCGCTCCGCATGGAGCGCCAGCGCCGCC 7445
 QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240

Db 7446 TCGGAGGAGAGAGAGCTGGCCAGCTTGCAGGTGCCTTATCACAGCTCTTCCAGAA 7505
Qy 241 TyrAspHisIleLysSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 7506 TACGACAAACACATCAAGAGAGCGCTGGTGGCAGTGCAGCGAGCGAGGATGCAGCTG 7565
Qy 261 GluAspLeuLysGlnGlnLeuGlnAlaGluAlaLeuValAlaLysGlnGluVal 280
Db 7566 GAGATCTCAACAGCAGCTCCAGCAGCGCCGAGGAGGCTTGGTGGCCAAACAGGAGGTG 7625
Qy 281 IleAspLysLeuLysGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db 7626 ATCGATAAGCTGAAGGAGGAGCGCCAGCAGCACAAAGATTGTGATGGAGACCGTTCGCGTG 7685
Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 7686 CTGAAGGCCCGAGGCGGATATCTCAAGCGGACTTCCAGGCTGAGAGCGAGGCCCGGAG 7745
Qy 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnLeuGlnLeuGlnArgGluTyr 340
Db 7746 AAGCTGCCCGAGAGAGGAGCTCTTCAGGAGCAGCTGGAGCAGCTGCAGAGGGAGTAC 7805
Qy 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
Db 7806 AGCAAACTGAAGGCCAGCTGTCAAGAGCTCGGCCAGGATCAGGAGACATGAGGAAGCGCAT 7865
Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaProAlaProAlaProAla 380
Db 7866 GTCAGAGTCTCCAGGCCCGCCCTTGCCTCCCGCCCGCCCTTGCCTCCCTCCCTCCGTC 7925
Qy 381 LeuProSerGlnArgArgSerProGluGluProGluProGluProGluProGluProGlu 400
Db 7926 CTGCCAGCCAG 7985
Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 7986 CAGTATCAGGCCCTGATATGGACACCCCTGCAGATACATGTCATGGAGTGCATTGAG 8042

RESULT 15

ABD20693
ID ABD20693 standard; DNA; 8631 BP.

AC ABD20693;
XX
XX
XX 29-JUL-2004 (first entry)
XX Human pulmonary and inflammatory target DNA #304.
DE
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antisthmatic;
KW analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
XX Homo sapiens.
XX
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX

DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 12086; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antisthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cycostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 8631 BP; 2280 A; 2051 C; 2270 G; 2030 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4, 95e-152 Length: 8631
Score: 2115.00 Matches: 419
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0
US-09-377-795-2 (1-419) x ABD20693 (1-8631)
Qy 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 6786 ATGAATAGGACCCCTCTGGAAGAGCCCACTCTGTGAGATGTCGAGCCAGTGGTGGCCG 6845
Qy 21 AlaAlaAspGlnAspValLeuGluGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 6846 GCAGCAGATCAGGACCGTACTTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 6905
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60
Db 6906 CTGCCTTCAGACAGAGGCGCTCTTGAGACCTTCAGCGCTGCTGGAGGAGATCAAGAG 6965
Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeu 80
Db 6966 CTCGAGATGCCATCCGCGAGAGCAACACAGATTCTCGGAGGCGCTCCGAGGAGCTTCTG 7025
Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
Db 7026 CATTTCCAGCCAGAGGAGAGAGAGAGTCTCTCATGTGCAAGTTCCAGGAGGCC 7085
Qy 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120

|||||
Db 7086 AGGAACTGGTGGAGAGCTCGGCTCGAGAGCTCGATCTGAGAGGCGAAGAGGACG 7145
QY 121 AlalaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
Db 7146 GCTCTGGCGAGGTGGAGACCTCAAGAGATGCCAGCAGCAGATGCTGAGGACAAGGCC 7205
QY 141 SerValLysAlaGlnValThrSerLeuLysGluGluGlnLysSerGlnSerArgLeu 160
Db 7206 TCTGTGAAGCCCAAGGTGAGCTCTTCTCGGGAGCTGCAGGAGGCCAGAGTGCCTTG 7265
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 7266 GAGGCTGCCACTAAGGAATGCCAGGCTCTGAGGGTCGGGCCCGGCCAGCGAGCAG 7325
QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGlnValAsp 200
Db 7326 GCGGGCAGCTGGAGAGTGAAGCGAGCGAGCGCTGCAGCAGCAGCACAGCGTGCAGGTGGAC 7385
QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 7386 CAGCTGGCATGCGAGGCCAGAGCGTGGAGCGCGCTCCGATGGAGCGCCAGGCCGCC 7445
QY 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
Db 7446 TCGAGGAGAGAGAGAAAGCTGGGCCAGTTGCAGGTGGCTATCACCGACTCTCCAGAA 7505
QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 7506 TACGACAAACACATCAAGAGCAGCGTGGTGGCAGTGAGCGGAAGCGAGGAATGCAGTG 7565
QY 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 7566 GAAGATCTCAACAGCAGCTCCAGCAGGCCGAGGAGGCCCTGGTGGCCAAACAGAGGTG 7625
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db 7626 ATCGATAAGCTGAAGGAGGAGCGGAGCAGCAGCACAGATTGTGATGGAGACCGTCCGGTG 7685
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 7686 CTGNAGGCCCGCGGATATCTACAAGCGGACTTCCAGGCTGAGAGGAGGCCCGGGAG 7745
QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnLeuGlnLeuGlnArgGluTyr 340
Db 7746 AAGCTGGCCGAGAAGAGAGCTCTCTGAGGAGCAGCTGCAGCAGCTGCAGAGGGAGTAC 7805
QY 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
Db 7806 AGCAAACTGAAGGCCAGCTGTCAAGGAGTCGGCCAGGATCGAGGACATGAGGAAGCGGAT 7865
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 7866 GTCGAGGTCTCCAGGCCCTTGGCCCCCGCCCTGCTACTCTCTCTCTCTCTCTCTCTCT 7925
QY 381 LeuProSerGlnArgSerProGluGluProProAspPheCysCysProLysCys 400
Db 7926 CTGCCAGCCAGAGGAGGAGCCCCCGGAGGAGCACCTGACTTCTGTCTCTCTCTCTCTCT 7985
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 7986 CAGTATCAGGCCCTGATATGGACACCTTCGAGATACATGTCATGAGTGCATTGAG 8042

Search completed: February 9, 2005, 03:30:18
Job time : 758 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 9, 2005, 02:52:33 ; Search time 4378 Seconds
(without alignments)

3642.971 Million cell updates/sec

Title: US-09-377-795-2

Perfect score: 2115

Sequence: 1 MNRLKWSQICVQPSGGP.....COYQAPDMDTLQIHVMCEIE 419

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh

-Q/cgn2_1/USPTO_spool/US09377795/runat_07022005_112551_12131/app_query.fasta_1.583

-DB=EST -Qfmt=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=1 -MATRIX=blowsum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US09377795 @CGN 1.1 4352 @runat_07022005_112551_12131 -NCPU=6 -ICPU=3

-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2115	100.0	1958	3	CR600010 full-leng
2	2115	100.0	1960	3	BC046922 Homo sapi
3	2099.5	99.3	1962	6	CA916723 K142FL hu
4	2086.5	98.7	1943	3	CR604149 full-leng
5	1840.5	87.0	1751	3	CR603029 full-leng
6	1813	85.7	4535	3	AK037020 Mus muscu
7	1412.5	66.8	1118	5	EX332283 BX332283
8	1322	62.5	974	1	AL545822 AL545822
9	1308.5	61.9	1043	1	AL541141 AL541141

10	1253.5	59.3	957	5	BQ932422	AGENCOURT
11	1247	59.0	919	1	AL547021	AL547021
12	1245.5	58.9	1098	4	BM478785	AGENCOURT
13	1235	58.4	1024	1	AL558226	AL558226
14	1225	57.9	1011	5	BX325316	BX325316
15	1208.5	57.1	920	5	BX418246	BX418246
16	1206	57.0	1098	4	BM473416	AGENCOURT
17	1205	57.0	975	5	BX418245	BX418245
18	1200	56.7	925	5	BX328265	BX328265
19	1194	56.5	902	5	BQ44161	AGENCOURT
20	1150	54.4	872	5	BX418606	BX418606
21	1135.5	53.7	1091	4	BM467195	AGENCOURT
22	1123.5	53.1	929	5	BU528711	AGENCOURT
23	1120	53.0	942	5	BU930960	AGENCOURT
24	1118.5	52.9	963	1	AL526920	AL526920
25	1093	51.7	788	7	CN460471	CN460471
26	1093	51.7	870	5	BQ956152	AGENCOURT
27	1090	51.5	1140	4	BM546491	AGENCOURT
28	1084	51.3	757	7	CO433136	UI-M-HXO-
29	1070	50.6	1051	5	BQ056837	AGENCOURT
30	1066.5	50.4	1056	5	BQ057044	AGENCOURT
31	1060	50.1	634	7	CV025468	CV025468
32	1055.5	49.9	730	5	BU708502	UI-M-F10-
33	1053	49.8	758	4	BI765235	603050326
34	1052.5	49.8	994	5	BQ716889	AGENCOURT
35	1045.5	49.4	781	7	CK639928	UI-M-HNO-
36	1045	49.4	951	5	BQ064520	AGENCOURT
37	1039	49.1	764	7	CN460413	CN460413
38	1027	48.6	1164	3	CR612085	full-leng
39	1023	48.4	781	5	BX398053	BX398053
40	1019.5	48.2	815	5	BX324969	BX324969
41	1014	47.9	923	4	BM559994	AGENCOURT
42	1011.5	47.8	686	7	CK636315	UI-M-HNO-
43	1010.5	47.8	733	5	BQ771466	UI-M-F10-
44	1008	47.7	789	6	CB521645	UI-M-GHO-
45	1001.5	47.4	1201	2	BE273489	601143504

ALIGNMENTS

RESULT 1	CR600010	1958 bp	linear	HTC 21-JUL-2004
LOCUS	CR600010	full-length cDNA clone CS0DL002VJ17 of B cells (Ramos cell line)		
DEFINITION	CR600010	Cot 25-normalized of Homo sapiens (human).		
ACCESSION	CR600010.1	GI:50480817		
VERSION	HTC; CNSLT CDNA.			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 1958)			
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue			
REFERENCE	2 (bases 1 to 1958)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)			
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime ends enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.			
FEATURES	Location/Qualifiers			
source	1..1958			
	/organism="Homo sapiens"			

COMMENT

Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mc@nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 44 Row: 1 Column: 23
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 21361093
 This clone has the following problem: frame shifted.

FEATURES

source

1..1960
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5476394"
 /tissue types="Skin, melanoma, amelanotic"
 /clone_lib="NIH MGC 41"
 /lab_host="DH10B-R"
 /note="Vector: pOTB7"

ORIGIN

Alignment Scores:
 Pred. No.: 5,09e-182 Length: 1960
 Score: 2115.00 Matches: 419
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-377-795-2 (1-419) x BC046922 (1-1960)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuGluMetValGlnProSerGlyGlyPro 20
 |||
 DB 116 ATGAATAGGCACCTCTGGAAGAGCAACTGTGTGAGATGGTGCAGCCAGTGGTGGCCG 175
 |||
 QY 21 AlaAlaaspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
 |||
 DB 176 GCAGCAGATCAGACGCTGAGGAGAGAGTCTCTCTGGGGAAGCCAGCATGCTGCAC 235
 |||
 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
 |||
 DB 236 CTGCCTTCAGAACAGGGCGCTCTTGAGACCTTCAGCGCTGCTGGAGGAGATCAAGAG 295
 |||
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
 |||
 DB 296 CTCGAGATGCCATCCGGCAGAGCAACACAGATTCTGCGGAGCGCTGCGAGGAGCTTCG 355
 |||
 QY 81 HisPheGlnIleSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
 |||
 DB 356 CATTTTCAAGCCAGCCAGAGGAGGAGAGAGTCTCTCATGTGCAAGTTCCAGGAGGCC 415
 |||
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
 |||
 DB 416 AGAAGACTGTGTGAGAGACTCGGCCTGGAGAGCTCGATCTGAAGAGGAGAGAGGAGCAG 475
 |||
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
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DB 476 GCTCTCGGAGGCTGGAGCACCTGAAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 535
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
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 DB 536 TCTGTGAAGCCAGGTGAGTCTCTTGTCTGGGAGAGCTGCAGGAGACCGAGTTCGTTG 595
 |||
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
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 DB 596 GAGGCTCCCACTAAGGAATGCCAGGCTCTGAGGGTCCGGCCCGGGCGGCGAGCAG 655
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 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
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 DB 656 GCGCGGCGAGCTGAGAGTGCAGCGAGGCGCTGCAGCAGCAGCAGCAGCTGCAGGTGCAC 715
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 QY 201 GlnLeuArgMetGlnGlnSerValGluAlaLeuAlaLeuArgMetGluArgGlnAlaAla 220
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 DB 716 CAGCTGCGCATGAGGCGCAGAGCGGTGGAGCGCGCTCCGCATGGAGCGCCAGGCGGCC 775
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 QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
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 DB 776 TCGGAGGAGAGAGGAGGAGCTGGCCAGTTGCAGGTGGCTTATCACCAGCTCTTCCAAGAA 835
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 QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
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 DB 836 TAGCAACACCATCAAGAGCAGCGTGTGGGCGAGTGCAGCGAAGCGAGGAGTGCAGCTG 895
 |||
 QY 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
 |||
 DB 896 GAAGATCTCAACAGCAGCTCCAGCAGGCGCGAGGCGCTTGTGGCCAAACAGGAGGTG 955
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 QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
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 DB 956 ATCGATAGCTGAAGGAGGAGGCGCGAGCAGCAGCACAAGATTGTGTGAGACCGTTCGGTG 1015
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 QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
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 DB 1016 CTGAAGGCCCGAGCGCATATCTACAAGGCGGACTTCAGGCTGAGAGGCGGCGGAG 1075
 |||
 QY 321 LysLeuAlaGluLysGluLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 340
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 DB 1076 AAGCTGGCGAGAGAGAGGAGTCTCTGCAGGAGCAGCTGGAGCAGCTGCAGAGGAGTAC 1135
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 QY 341 SerLysLeuLysAlaSerCysGlnGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
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 DB 1136 AGCAACTGAAGCCAGCTGTCAAGAGTCCGCCAGGATCGAGGACATGAGAGCGGCAT 1195
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 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
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 DB 1196 GTCGAGGTCTCCAGGCGCCCTTGGCCCGCCCTGCTACCTCTCTCTCCCTCGGCC 1255
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 QY 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400
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 DB 1256 CTGCCAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 415
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 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
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 DB 1316 CAGTATCAGGCGCTGATATGAGACCTTCAGATACATGTCATGAGTGCATGAG 1372
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RESULT 3
 CA916723
 LOCUS
 DEFINITION
 1962 bp mRNA linear EST 14-MAR-2003
 K142PL human keratinocyte matchmaker cDNA library Homo sapiens CDNA
 clone K142 5' similar to IKK gamma/ NEMO, mRNA sequence.

ACCESSION
 CA916723
 VERSION
 CA916723.1 GI:28951960
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1962)
 Scaraflia, L.E., Stouffer, S.D. and Swinney, D.C.
 Identification of Ring Finger proteins that interact with Ubch5a,
 TITLE

JOURNAL
COMMENT

an ubiquitin-conjugating enzyme
Unpublished (2002)
Contact: Scarafia LE
Enzymology

Roche Bioscience
3401 Hillview Ave, S3-1, Palo Alto, CA 94304-1397, USA
Tel: 650 354 7997
Fax: 650 354 7554
Email: liliana.scarafia@roche.com
Full length single stranded sequencing of baited insert
Insert Length: 2000 Std Error: 0.00
Seq primer: primer 2 (5395)TACCACCTACAATGGATG; and insert-specific
POLYA=Yes.

FEATURES
source

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="K142"
/cell_type="keratinocyte"
/cell_line="HaCat cell line; derived from long term primary
human adult skin keratinocyte"
/lab_host="yeast/E.coli"
/clone_lib="human keratinocyte matchmaker cDNA library"
/note="Vector: pACT2; Site 1: EcoRI; Site 2: XhoI;
Matchmaker yeast two-hybrid system from Clontech; pACT2
vector has GAL4 AD and HA epitope under ADH1 promoter.
This oligo-dr primed library was screened with human
UbCH5a as bait, to obtained interacting proteins."

ORIGIN

Alignment Scores:
Pred. No.: 1 32e-180 Length: 1962
Score: 2099.50 Matches: 418
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.76% Mismatches: 0
Query Match: 99.27% Indels: 1
DB: 6 Gaps: 1

US-09-377-795-2 (1-419) x CA916723 (1-1962)

Qy 1 MetanArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 126 ATGAATAGGACCTCTGGAAGACCACTGTGTGAGATGTCAGCCAGTGGTGGCCGG 185

Qy 21 AlaAlaSerGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 186 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 245

Qy 41 LeuProSerGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
Db 246 CTGCTTCAGAACAGGGCGCTCTGAGACCTCCAGCCGCTGCTGGAGAGATCAAGAG 305

Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80
Db 306 CTCGAGATGCCATCCGGCAGAGACCACTGTCGGGAGCGCTGCGAGAGCTTCTG 365

Qy 81 HisPheGlnAlaSerGlnArgGluGlyGluPheLeuMetCysLysPheGlnGluAla 100
Db 366 CATTTCCAGCCAGCCAGAGGAGGAGAGAGTTCCTCATGTGCAAGTTCAGAGAGGCC 425

Qy 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 426 AGCAAACTGTGGAGAGACTCGCCCTGGAGAGCTCGATCTGAAGAGCCAGAGAGAG 485

Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
Db 486 GCTCTCGGGAGGTGGAGACCTGGAAGATGC---CAGCAGATGGCTCAGGACAAGGCC 542

Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerGlnSerArgLeu 160
Db 543 TCTGTGAAGCCAGGTGACGTCTTGTCTGGGGAGCTGCAGGAGCCAGAGTCGCTTG 602

Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaSerGluGln 180
Db 603 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGGCCCGGCGCCAGCGAGCAG 662

Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGlnValAsp 200
Db 663 GCGCGCAGCTGGAGAGTGAGCGCGCTGTCAGCAGCAGCAGCAGCAGCTTCAGGTTGGAC 722

Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 723 CAGCTGCGCATGCGAGGCCAGAGCGTGGAGGCGCGCTCCGATGGAGCGCCAGCGCGCC 782

Qy 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaIleTyrHisGlnLeuPheGlnGlu 240
Db 783 TCGGAGGAGAAAGAGGAGCTGGCCAGTTGCGAGTGGCTATCACAGCTCTTCCAGAA 842

Qy 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 843 TACGACCAACCATCAAGAGCAGCGTGTGGCAGTGGAGCGGAAGCGAGGAATGCGAGT 902

Qy 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 903 GAAGATCTCAACAGCAGCTCCAGCAGCCCGCAGGAGGCCCTGGTGGCCAAACAGGAGGT 962

Qy 281 IleAspLysLeuLysGluGluAlaGlnHisLysIleValMetGluThrValProVal 300
Db 963 ATCGATAGCTGAAGAGGAGCGCGCAGCAGCAGCAAGATTGTGATGGAGACCTTCGGGT 1022

Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 1023 CTGAGGCCCGCGCGATATCTACAGCGGAGCTTCAGGCTGAGAGGAGCCCGGGAG 1082

Qy 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnLeuGlnGluGlnArgGluTyr 340
Db 1083 AAGCTGGCCGAGAAGAGGAGCTCTTCAGGAGCAGCTGGAGCAGCTGCAGAGGAGTAC 1142

Qy 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
Db 1143 AGCAAACTGAAGGCCAGCTGTTCAGAGTTCGCGCAGGATCGAGGACATGAGGAAGCGGCAT 1202

Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 1203 GTCCAGGTCTCCAGGCCCTTCGCCCGCCCTGCTGCTACCTCTCTCTCTCCCTGGCC 1262

Qy 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400
Db 1263 CTGCCCAGCAGAGGAGAGGCCCGCCGAGAGCCACTGACTTCTGCTGTCTCCCAAGTGC 1322

Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 1323 CAGTATCAGGCCCTGTATATGGACACCTTCAGATACATGTCAGTGGAGTGCATTGAG 1379

RESULT 4
CR604149
LOCUS full-length cDNA clone CS0DE005YJ20 of Placenta of Homo sapiens
DEFINITION full-length cDNA clone CS0DE005YJ20 of Placenta of Homo sapiens (human).
ACCESSION CR604149
VERSION CR604149.1 GI:50484956
KEYWORDS HTC; CNSLT; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 1943)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE 2. (bases 1 to 1943)
Genoscope.

TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES Location/Qualifiers
 source 1..1943
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DE005YJ20"
 /tissue_type="Placenta"
 /plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
 Pred. No.: 2e-179 Length: 1943
 Score: 2086.50 Matches: 419
 Percent Similarity: 99.52% Conservative: 0
 Best Local Similarity: 99.52% Mismatches: 0
 Query Match: 98.65% Indels: 2
 DB: 3 Gaps: 1

US-09-377-795-2 (1-419) x CR604149 (1-1943)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
 Db 137 ATGAATAGGACCTCTGGAGAGCCAACTGTGTGAGATGTGTGAGCCAGCCAGTGTGTCGCCG 196

QY 21 AlaAlaAspGluAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
 Db 197 GCAGCAGATCAGACGCTACTGGCGGAAGAGTCTCTCTGGGAAGCCAGCCATGTGTCAC 256

QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
 Db 257 CTGCCTTCAGACAGCGCGCTCTTGAGACCTCCAGCGCTGCTGGAGGAGATCAAGAG 316

QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
 Db 317 CTCAGAGATGCCATCCGCGAGACCAACAGATTCCTGCGGAGCGCTGCGAGGAGCTTCG 376

QY 81 HisPheGlnAlaSerGlnArgGluGlyGluPheLeuMetCysLysPheGlnGluAla 100
 Db 377 CATTTCCAAAGCCAGCCAGAGGAGGAGAGGAGTTCCTCATGTGCAAGTTCAGAGAGGCC 436

QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
 Db 437 AGGNAACCTGGTGAGAGACTCGCCCTGGAGAGCTCGATCTGAGAGGCGAGAGGAGCAG 496

QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
 Db 497 GCTCTGCGGGAGGTGGAGCACCTGAAGAGATGCCAGCAGCAGATGCTGAGCACAAGGCC 556

QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
 Db 557 TCTGTGAAAGCCAGGTGACGCTCTGTCTGCGGGAGCTCAGAGAGCCAGAGTGCCTTG 616

QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
 Db 617 GAGGCTGCCACTAGGAATGCCAGGCTCTGGAGGGTGGGGCCCGGCGCCAGCAGCAG 676

QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
 Db 677 GCGCGCAGCTGGAGAGTGGCGGAGCGCTGTCAGCAGCAGCAGCAGCTGTCAGGTGGAC 736

QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
 Db 737 CAGCTGCGCATCAGGCGCCAGAGCGGTGGAGGGCCGCGCTCCGATGAGCGCCAGCGCCG 796

QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
 Db 797 TCGGAGGAGAGCAGAGAGCTGCCCCAGTTGCGAGTGGCCCTATCACAGCTCTTCCAAGAA 856

QY 241 TyrAspAsnHisIleLysSerSerValValGlyLysArgLysArg----GlyMetGlu 259
 Db 857 TAGCAACACCATCAAGAGCAGCGTGGTGGCGAGTGGAGCGAAGCAGTGGAGGAATGCA 916

QY 259 nLeuGluAspLeuLysGlnGlnGlnAlaGluGluAlaLeuValAlaLysGlnGlu 279
 Db 917 GCTGGAAGATCTCAAAACAGCAGCTCAGCAGCGCCGAGGAGGCCCTGGTGGCCAAACAGGA 976

QY 279 uValIleAspLysLeuLysGluAlaGluGlnHisLysIleValMetGluThrValPr 299
 Db 977 GGTGATCGATAAGCTGAAGAGGAGCGCCGAGCAGCAGCAAGATTGTGATGGAGACCGCTTC 1036

QY 299 oValLeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaAr 319
 Db 1037 GGTGCTGAAGGCCAGGCGGATATCTACAAGCGGAGCTTCCAGGCTGAGAGGCGAGCCCG 1096

QY 319 gGluLysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGluGlnLeuGlnArgGlu 339
 Db 1097 GGAGAAGCTGGCCGAGAGAGAGAGCTCTCTGAGGAGCAGCTGGAGCAGCTGCAGAGGGA 1156

QY 339 uTyrSerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysAr 359
 Db 1157 GTACAGCAAACTGAAGGCCAGCTGTGAGAGTCCGCCAGGATCGAGGACATCAGGAAGCG 1216

QY 359 gHisValGluValSerGlnAlaProLeuProProAlaTyrLeuSerSerProLe 379
 Db 1217 GCATGTCGAGGTCTCCAGGCGCCCTTGCCCCCGCCCTGCTCTCTCTCTCTCTCTCTCT 1276

QY 379 uAlaLeuProSerGlnArgArgSerProGluGluProProAspPheCysProLys 399
 Db 1277 GGCCCTGCCAGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1336

QY 399 sCysGlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
 Db 1337 GTGCCAGTATCAGGCGCCCTGATATGACACCTGTCAGATACATGTCATGAGTGCATTGA 1396

QY 419 u 419
 Db 1397 G 1397

RESULT 5
 CR603029 full-length cDNA clone CS0DC017YA10 of Neuroblastoma Cot 25-normalized of Homo sapiens (human).
 LOCUS CR603029.1 GI:50483836
 DEFINITION HTC; CNSLT_cDNA.
 ACCESSION CR603029
 VERSION HTC; CNSLT_cDNA.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1751)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue
 REFERENCE 2 (bases 1 to 1751)
 Genoscope.
 Direct Submission
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 JOURNAL

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.
Location/Qualifiers
source
1. 1751
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC017A10"
/tissue type="Neuroblastoma Cot 25-normalized"
/plasmid="PCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.: 4,76e-157 Length: 1751
Score: 1840.50 Matches: 368
Percent Similarity: 87.83% Conservatives: 0
Best Local Similarity: 87.83% Mismatches: 0
Query Match: 87.02% Indels: 51
DB: 3 Gaps: 1

US-09-377-795-2 (1-419) x CR603029 (1-1751)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
DB 128 ATGAATAGGACCTCTGGAGAGCCAACTGTGTGAGATGGTCAGCCAGTGGTGGCCG 187
QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
DB 188 GCAGCAGATCAGGACGCTACTGGCGAGAGTCTCTCTGGGAGACCCAGCCATGCTGCAC 247
QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
DB 248 CTCCCTTCAGAACAGAGGCGCTCTGAGACCTCCAGCGCTGCTGAGGAGCAATCAAGAG 307
QY 61 LeuArgAspAlaIleArgGlnSerLeuGlnLeuArgGluArgCysGluGluLeuLeu 80
DB 308 CTCGAGATGCCATCCGAGAGACCAACAGATCTGCGGAGCGCTGCGAGAGCTCTG 367
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
DB 368 CATTTCCAGCCAGCCAGAGGAGAGAGGAGTCTCTCATGTGCAGTTCAGAGAGGCC 427
QY 101 ArgLysLeuValGluArgGluGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
DB 428 AGGAACACTGGTGAGAGACTCGCGCTGGAGAGCTCGATCTGAAGAGGAGCAGAGGAGCAG 487
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
DB 488 GCTCTGCGGAGGTGGAGCACTTGAGAGATGCCAGCAGATGGCTGAGGACAGGCC 547
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
DB 548 TCTGTGAAGCCAGGTGACGTCCTTGCTCGGGAGCTGTCAGGAGAGCCAGAGTCGCTTG 607
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
DB 608 GAGGCTGCCACTAGAGATGCCAGGCTCTGGAGGCTCGG----- 646
QY 181 AlaArgGlnLeuGluSerGluGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
DB 646 ----- 646
QY 201 GlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
DB 646 ----- 646
QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
DB 647 -----AGGAACCTGGCCAGTTCGAGGTGGCTATCACAGCTCTTCCAGAA 694
QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
DB 695 TACGACAAACCATCAAGAGCAGCGTGTGGGAGTGGAGGAGGAGCAATGCAGCTG 754

QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
DB 755 GAAGATCTCAACAGCAGCTCCAGCAGCCGAGGAGGCGCTGGTGCACCAACAGAGGAGTG 814
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
DB 815 ATCATTAAGCTGAAGGAGGAGGCGCAGCAGCAGCAAGATTGTGATGGAGACCTTCGGGTG 874
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
DB 875 CTGAGGCCCGAGCGGATATCTAAGCGGAGCTTCAGGCTGAGAGGAGGCCCGGGAG 934
QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnGlnLeuArgGluTyr 340
DB 935 AAGCTGGCCGAGAGAGAGGAGCTCTGTCAGGAGCAGCTGGAGCAGCTCAGAGGCGAGTAC 994
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerLysAlaArgIleGluAspMetArgLysArgHis 360
DB 995 AGCAACTGAAGCCAGCTGTGAGAGTGGCGGAGGATCGAGGACATGAGGAAGCGCAT 1054
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLeuSerSerProLeuAla 380
DB 1055 GTCAGGCTCTCCAGGCGCCCTTGCCGCCCGCCCTGCTACCTCTCTCTCTCTCTCTCT 1114
QY 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400
DB 1115 CTGCCCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1174
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
DB 1175 CAGTATCAGGCCCTTGATATGAGCAGCCCTGACAGATACATGTATGAGAGTGCATTGAG 1231

RESULT 6
AK037020 4535 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult female vagina cDNA, RIKEN full-length enriched
DEFINITION library, clone:9930039F20 product:unknown EST, full insert
sequence.
ACCESSION AK037020
VERSION AK037020.1 GI:26331883
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujisaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4

AUTHORS
JOURNAL
REFERENCE
AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4535)

TITLE
JOURNAL
REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Iotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

TITLE
JOURNAL

1. .4535
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:9930039F20"
/db_xref="taxon:10090"
/clone="9930039F20"
/sex="female"
/tissue_type="vagina"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
136. .1371
/dev_stage="adult"
/notes="unnamed protein product; putative unknown EST (GB|BB646967, evidence: BLASTN, 99%, match=720)"
/codon_start=1
/protein_id="BAC29672.1"
/db_xref="GI:26331884"
/translation="MNKHFWKNQLESMVOPSGPAPEDQMLGEESLKGPKAMHLHPSE QGTPETLQCLENDELDAIRQSNQMLRERCEELHDFQVSRKEEFKLMCKFPQARK LVERLSLEKDLRSOREQALKEQLKKCCQQAEDKASVKAQVTSLLGELOESQRLE AATKROALEGRIRAVSROVLESEREVLOQHSVQVDVLRMONQSVFAALRMEROA ASEERKKAQLQAQVHQLFQDYDSHTKSSKGQLEDLRLQQLQAQSEALVAKQELDKL KEAQQHKLVMETVPVFKQAQADLYKADFOAERHAREKLVVEKKEYLOEQLQREBFLK LKVGCHESARIEDMRKRHVETPQPLLPAPAHSHFLALSNNQRSPPEPFPDFCCPKC QCAQMDMDLQIHHVMECIE"

COMMENT

polya_signal
4515. .4520
/note="putative"
polya_site
4535
/note="putative"

FEATURES
source

ORIGIN
Alignment Scores:

CDS

Pred. No.:	5.63e-154	Length:	4535
Score:	1813.00	Matches:	362
Percent Similarity:	90.93%	Conservative:	19
Best Local Similarity:	86.40%	Mismatches:	30
Query Match:	85.72%	Indels:	8
DB:	3	Gaps:	2
US-09-377-795-2 (1-419) x AK037020 (1-4535)			
QY	1	MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro	20
DB	136	ATGAACAAGACACCCCTGGGAAGAACCAAGCTGAGTGGTGGAGATGGTGGAGCCCTGGTGGCCCA	195
QY	21	AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis	40
DB	196	GCAGAGGACCAAGACATGCTGGGTGAAGAACTCTCTCTGGGAGAGCTGCATGCTACAT	255
QY	41	LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGlnGluGlu	60
DB	256	CTGCCTTCAGACGAGGCTACTCTGAGACCTCCAGCGCTGCTGGAAGAAATCAAGAG	315
QY	61	LeuArgAspAlaIleArgGlnSerHisGlnIleLeuArgGluArgCysGluGluLeu	80
DB	316	CTCCGAGACGCTATCCGCGAGACCAATCAGATGCTGAGGGAACGCTGTGAGGAGCTGCTG	375
QY	81	HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla	100
DB	376	CATTTCCAGTCAGCCGCGGAGAGAGAGAGTTCCTTATGTGCANAATTCAGGAGGCC	435
QY	101	ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln	120
DB	436	CGGAAGCTGGTGGAGAGACTGAGCTTGGAGAAGCTTGATCTTCGAGTCAGAGGGAACAG	495
QY	121	AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla	140
DB	496	GCTTTAAAGGAGTGGAGCAACTGAAGAAATGC---CAACAGATGCTCAGGACCAAGGCC	552
QY	141	SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu	160
DB	553	TCTGTGAAGCTCAGGTGACATCATCTGCTCGAGAACTCCAGAGAGCCAGAGCCGTTTG	612
QY	161	GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaSerGluGln	180
DB	613	GAGGCTGCCACCAAGATCGGCAAGCTTTAGAGGGAAGGATTCGAGCAGTTAGTGAGCAG	672
QY	181	AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp	200
DB	673	GTCAACAGCTGGAGAGTGAGCGGAGGTGCTTACAGCAGCAGCAGCAGCTCCAGGTGGAC	732
QY	201	GlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla	220
DB	733	CAGCTCGGTATGCCAACCAGAGCGTGGAGGCTGCTTCCGAATGGAGCGGCGAGGCTGCT	792
QY	221	SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu	240
DB	793	TCAGAGGAGAACGCGAAGCTGGCTCAGTTGAGGAGCGCTATCACCAGCTCTTCCAAGAC	852
QY	241	TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu	260
DB	853	TACGACAGCACATTAAGACGAC-----AAGGCGATGACAGCTG 891	
QY	261	GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal	280
DB	892	GAAATCTGAGGCAACAGCTCCAGAACGCTGAGGAGGCGCTGGTATGCCAACAAGAAATTT	951
QY	281	IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal	300
DB	952	ATTGATAGCTGAAGAGGAGGCTGAGCAGCAGCAAGATTTGATGAGAGCTGTGCCAGTC	1011
QY	301	LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu	320
DB	1012	TTGAAGGCGCCAGCGGATATCTACAAGGCTGACTTCCAAGCTGAGAGGATGCCCGGAG	1071

QY		LysLeuAlaGluLysLysGluLeuLeuGlnGlnLeuGluGlnArgGluTyr	340
Db		AAAGCTGGTGGAGAAGAAGGATATTTCAGACGACACTGCAGCGCAGTTC	1131
QY		SerLysLeuLysAlaSerCysGlnGlnSerAlaAqIleGluAspMetArgLysArgHis	360
Db		AAAAGCTGAAGTTGGCTGCCATGAGTCAGCCAGGATTTAGGATATGAGGAGCGGCAT	1191
QY		ValGluValSerGlnAlaProLeuProToAlaProAlaTyLeuSerSerProLeuAla	380
Db		GTAGAGACTCCCCAGCCTCCTTACTCCCTGTCTCCAGCTCACCACTCCTTTTCATTGGCC	1251
QY		LeuProSerGlnArgArgSerProCgLuGluProProAspPheCysCyvProLysCys	400
Db		TGTGCCAACCGAGGAGGAGCCCTCCTTGAGAACTCTCTGACTCTCTGTGTCCGAGTGC	1311
QY		GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysileGlu	419
Db		CAGTATCAGGCTCTGTAATGGACACTTACAGATACATGTCATGGATGCATAGAG	1368

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Alignment Scores:
Pred. No.:      2.82e-118
Score:          1410.50
Percent Similarity: 93.96%
Best Local Similarity: 93.35%
Query Match:    66.78%
DB:             5
length:         1118
Matches:        309
Conservative:   2
MismatchChes:  17
Indels:         7
Gaps:          0

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ACCESSION AL545822
VERSION AL545822.3 GI:45746298
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 974)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31267657.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10873.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE005DE100P1&c=10873.f.
FEATURES
source
1..974
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI023YC04"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 4,19e-110 Length: 974
Score: 1322.00 Matches: 275
Percent Similarity: 97.54% Conservative: 2
Best Local Similarity: 96.83% Mismatches: 5
Query Match: 62.51% Indels: 3
DB: 1 Gaps: 0
US-09-377-795-2 (1-419) x AL545822 (1-974)
QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 126 ATGAATAGGCACCTCTGGAARAGCCAACTGTGTGARATGTTGCAGCCCACTGTCGCCG 185
QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 186 GCAGCAGATCAGACGCTACTGGCGGAAGAGTCTCTCTCGGGAAGCAGCCATGCTGCAC 245
QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGlnGlnGlu 60
Db 246 CTGCCTTCAGAACAGGGCGCTCTGAGACCCCTCCAGCGCTGCTGGAGGAGATCAAGAG 305
QY 61 LeuArgAspAlaIleArgGlnSerAenGlnIleLeuArgGluArgCysGluGluLeu 80
Db 306 CTCGAGATGCCATCCGGCAGACCAACAGATTCTCGGGAGCGCTGCAGGAGCTTCTG 365
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
Db 366 CATTTTCAAGCCAGCCAGAGGGAGGAGAGGAGTTCTCTATGTCGAAGTTCCAGGAGGCC 425
QY 101 ArgLysLeuValGluArgGluGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 426 AGGAACCTGGTGAGAGACTCGCGCTGGGAGAGCTCGATCTGAAGAGGAGGAGGAGCAG 485
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140

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Db 486 GCTCTGCGGGAGGTGGAGCACCTGAAGAGATGCCAGCAGCAGATGCTGAGACAAGGCC 545
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
Db 546 TCTGTGAAGCCAGGTGACGTCCTTGTCTCGGGAGCTGCAGGAGAGCCAGAGTTCGCTTG 605
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 606 GAGGTGCTCCACTAAGGATGCCAGGCTCTGGAGGGTTCGGCCCGGGCCGAGGAGCAG 665
QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGln-ValAs 200
Db 666 GCGCGCAGCTGGAGATGAGCGCGAGCGCTGCAGCAGCAGCAGCAGCGTGCAGGGTGA 725
QY 200 pGlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAla 220
Db 726 CCAGCTGCGCATGCGAGGGCCAGAGCGTGGAGCGCGCTCCCGCATGGAGGCCAGGCGCC 785
QY 220 aSerGlu-GluLysArgLysLeuAlaGlnLeuGlnValAlaValHisGlnPheGlnG 240
Db 786 CTCGGAGGAGAGAGAGAGCTGGSCCAGTTGCAGGTGGCCTATCACCAGCTCTTCCAAG 845
QY 240 luTyAspAsnHisIleLysSerValValGlySerGluArgLysArgGlyMetGlnL 260
Db 846 AATACGACAAACCATCAAGCAGCAGCGTGGCGAGTGCAGCGGAASAGYGAATGCAGC 905
QY 260 euGluAspLeuLysGlnGlnGlnGlnAlaGluGluAlaLeuValAlaLysGlnGlu 280
Db 906 TGGAGATCTCAACAGCAGCTCCAGCAGCGCGAGGAGGCGCTGGTGGC-AAACAGGAGG 964
QY 280 alileAsp 282
Db 965 TGATCGAT 972

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RESULT 9
AL541141
LOCUS AL541141
DEFINITION AL541141 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE005YJ20
5-PRIME, mRNA sequence.
ACCESSION AL541141
VERSION AL541141.3 GI:45716735
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1043)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:30545027.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 10873.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE005DE100P1&c=10873.f.
FEATURES
source
1..1043
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE005YJ20"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed

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with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 7,84e-109 Length: 1043
Score: 1308.50 Matches: 278
Percent Similarity: 95.25% Conservative: 3
Best Local Similarity: 94.24% Mismatches: 13
Query Match: 61.87% Indels: 5
DB: 1 Gaps: 0

US-09-377-795-2 (1-419) x ALS41141 (1-1043)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
DB 139 ATGAATAGGACCTCTGGAAGACCACTGTGTGAGATGTCAGCCAGTGTGGCCGG 198
QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
DB 199 GCAGCAGATCAGACGCTACTGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 258
QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
DB 259 CTGCTTCAGAACAGGCGCTCTGAGACCTCCAGCGCTGCTGAGAGAGATCAAGAG 318
QY 61 LeuArgAspAlaLeuArgGlnSerLeuGlnLeuLeuArgGluArgCysGluLeuLeu 80
DB 319 CTCGAGATGCCATCCGCGAGACCAACAGATTCTCGCGGAGCGTGCAGAGAGCTTCTG 378
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
DB 379 CATTTCCAGCCAGCCAGAGGAGAGAGAGAGTTCCTCATGTGCAAGTTCAGAGAGCC 438
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
DB 439 AGAAACTCGTGAGAGACTCGGCTGGAGAGTCTGATCTGAAGAGGACAGAGAGCAG 498
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
DB 499 GCTTCGCGGAGGTGAGACCTCTGAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 558
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
DB 559 TCTGTGAAGCCAGGTGAGCGTCTTGTCTCGGGAGCTGCGAGAGAGCCAGATCGCTTG 618
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeu-GluGlyArgAlaAlaAlaSerGluGln 180
DB 619 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGADGGGTGGGCGCGCGCCAGCAGCA 678
QY 180 nAlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAs 200
DB 679 GCGCGGCGAGCTGAGAGTGGAGCGGAGGSGTG-CAGCAGCR-CACAGCGTGAGGTGGA 736
QY 200 pGlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAl 220
DB 737 CCAGCTGGCGATCGCGGCGCAGAGCGTGGAGCGCGCTCGCATCGGASCAAGGCGCG 796
QY 220 aSerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyHisGlnLeuPheGlnGln 240
DB 797 CTCGAGAGAGAGAGAGAGTGGCGCCAGTTCAGGTGGCCCTATCACCAGCTCTTCCAAGA 856
QY 240 uTyRAspLeuHisLeuLysSerSerValValGlySerGluArgLysArgGlyMetGlnLe 260
DB 857 ATACGACACACATCAAGACAGCGTGTGGTGGAGTGAGCGGAGGAGGAGATGAGCT 916
QY 260 uGluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVa 280
DB 917 GGAAGATCTCAAAACARCAAGCTCCAGCAGCGCGGAGGCGCCCTGGTGGCMAAMAGAGGT 976
QY 280 lIleAspLysLeuLysGluGluAlaGluGlnHisLysIleVal 294

Db 977 GATCGATAARCTGAAGGAGGG-GCCGAGMR-CACAAAATTTR 1017
|||||

RESULT 10

BQ932422

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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BQ932422 957 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8774276 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6375422
5', mRNA sequence.

BQ932422
BQ932422.1 GI:22347740

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 957)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LNCM2555 row: p column: 15

High quality sequence stop: 621.

Location/Qualifiers

FEATURES

source

1..957

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6375422"

/tissue_type="normal pigmented retinal epithelium"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_43"

/notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald W. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library. |"

Alignment Scores:

Pred. No.: 7,24e-104 Length: 957

Score: 1253.50 Matches: 253

Percent Similarity: 95.86% Conservative: 2

Best Local Similarity: 95.11% Mismatches: 10

Query Match: 59.27% Indels: 1

DB: 5 Gaps: 1

US-09-377-795-2 (1-419) x BQ932422 (1-957)

QY

1

MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20

DB

124

ATGAATAGGACCTCTGGAAGAGCCAACTGTGTGAGATGTCAGCCAGTGTGGCCGG 183

QY

21

AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40

DB

184

GCAGCAGATCAGACGCTACTGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 243

QY

41

LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60

DB

244

CTGCTTCAGAACAGGCGCTCTTCAGACCTCCAGCGCTGCTGGAGAGATCAAGAG 303

QY

61

LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80

RESULT 12
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 LOCUS AGENCOURT 6400582 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5526874
 DEFINITION 5', mRNA sequence.
 ACCESSION BM478785
 VERSION BM478785.1 GI:18527827
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1098)
 AUTHORS NTH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/BTP
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12201 row: d column: 11
 High quality sequence stop: 612.
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 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5526874"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Alignment Scores:
 Pred. No.: 4,69e-103 Length: 1098
 Score: 1245.50 Matches: 259
 Percent Similarity: 91.64% Conservative: 15
 Best Local Similarity: 86.62% Mismatches: 21
 Query Match: 58.89% Indels: 4
 DB: 4 Gaps: 3

US-09-377-795-2 (1-419) x BM478785 (1-1098)

QY 1 MetAsnArgHisLeuTriLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
 DB 132 ATGATAGGCACCTCTGGAAGAGCAACTGTGAGATGGTGACCGACGATGGTGGCCCG 191
 QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
 DB 192 GCAGCAGATCAGGAGCTACTGGGGAAGAGTCTCTCTGGGGAAGCCAGCATGCTGCAC 251
 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAenGlnGlu 60
 DB 252 CTGCGCTTCAGAACAGGGCGCTCTGAGACCTCCAGCGCTCGCTGGAGGAGAAATCAAGAG 311
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
 DB 312 CTCGAGATGTCATCCGCGAGCAACAGATTCCTGGGAGGCGCTGGAGGAGCTTCG 371
 QY 81 HisPheGlnAlaSerGlnArgGluGluysGluPheLeuMetCysLysPheGlnGluAla 100
 DB 372 CATTTCCAAAGCCAGCCAGAGGAGGAGAGAGTTCCTCATGTGCAAGTTCAGGAGGCC 431

QY 101 ArgLysLeuValGluArgLeuGlyLeuGlyLeuAspLeuLysArgGlnLysGluGln 120
 DB 432 AGGAAACTGGTGGAGAGACTCGGCTCGGAAAGCTCGATCTGAAGAGGAGGAGGAGCAG 491
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
 DB 492 GCTCTGGGGAGGTGGAGACCTGAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 551
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
 DB 552 TCTCTGAAAGCCAGGTGACCTCTCTCGGGAGCTGCGAGGAGCAGCAGATGCGCTTG 611
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
 DB 612 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGTGGGGCCGGCCGCGCAGCAGCAG 671
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
 DB 672 CGCGGCGAGCTGGAGAGTGAGCGCGAGCGCTGCGAGCAGCAGCAGCAGCGTGCAGTGGAC 731
 QY 201 GlnLeuArgMetGlnGlyGln-SerValGluAlaAlaLeuArgMetGluArgGlnAlaAl 220
 DB 732 CAGCTGGCATGCGAGGCGCAGAAACGCTGGAGGCGCGCTCGCATGAGCGCCAGGCCG 791
 QY 220 aSerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGln 240
 DB 792 CTGGAGGGGAGAGAAGAGCTGCCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 851
 QY 240 uTyrAspAsnHisIleLysSerValValGlySerGlu---ArgLysArgGlyMetGln 259
 DB 852 ATAGCACCACCTCCAGAAACACCGGTGGGCGAGTGGCGGAGCCGAGCCAGAAATGCAC 911
 QY 259 nLeuGluAspLeuGlnGlnLeuGlnAlaGluGluAlaLeuValAla---LysGln 278
 DB 912 CTGGAATAATCTCAACAGCAGCTCCACAGGCAAGAAAGCCCTGGGGGCCCCAACCG 971
 QY 278 nGluValIleAspLysLeu---LysGluGluAlaGluGlnHisLysIleValMet 295
 DB 972 GGAGGGGGTCCAAAACCTTAAGGAGGGAGGAGGAGCAACACCACCAAAATTTGATT 1026

RESULT 13
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 LOCUS AL558226 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 DEFINITION Homo sapiens cDNA clone CS0DJ001YH07 5-PRIME, mRNA sequence.
 ACCESSION AL558226
 VERSION AL558226.3 GI:46183625
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1024)
 AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:31280025.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 10873.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?S=CS0DJ001CD04QP1&c=10873.f.
 Location/Qualifiers
 1..1024
 /organism="Homo sapiens"
 /mol_type="mRNA"

FEATURES
 source


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/db_xref="taxon:9606"  
/clone="CS0DJ001YH07"  
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"  
/cell_line="JURKAT"  
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT  
10-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

Alignment Scores:
Pred. No.: 3.87e-102 Length: 1024
Score: 1235.00 Matches: 250
Percent Similarity: 98.43% Conservative: 1
Best Local Similarity: 98.04% Mismatches: 3
Query Match: 58.39% Indels: 1
DB: 1 Gaps: 0

US-09-377-795-2 (1-419) x AL558226 (1-1024)

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QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
DB 111 ATGAATAGGACCTCTGGAAGAGCAACTGTGTGAGATGTCGAGCCCAAGTGTGCGCG 170  
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QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeu 80  
DB 291 CTCGAGATGCCATCCGGCAGACCAACAGATTTCTCGGGAGCGCTGCAGGAGCTTCG 350  
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QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnSerGlnSerArgLeu 160  
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QY 200 pGlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAl 220  
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QY 220 aSerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaIleArgHisGlnLeuPheGln 240  
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RESULT 14
BX325316
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BX325316 1011 bp mRNA linear EST 07-APR-2004
Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL002YU17 5-PRIME, mRNA sequence.
BX325316
EST.
BX325316.2 GI:46265127
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1011)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 1, 2003 this sequence version replaced gi:30309451.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Crenieux, Cp 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10873.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0AL002CE09QPl&c=10873.f.

Location/Qualifiers

1. .1011

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/db_xref="taxon:9606"

/clone="CS0DL002YU17"

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25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 3.1e-101 Length: 1011
Score: 1225.00 Matches: 260
Percent Similarity: 94.22% Conservative: 1
Best Local Similarity: 93.86% Mismatches: 12
Query Match: 57.92% Indels: 5
DB: 5 Gaps: 0

US-09-377-795-2 (1-419) x BX325316 (1-1011)

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QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
DB 145 ATGAATAGGACCTCTGGAAGAGCAACTGTGTGAGATGTCGAGCCCAAGTGTGCGCG 204  
QY 21 AlaAlaAspAlaValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40  
DB 205 CGCAGCAGATCAGGACGTACTGGCGAAGAGTCTCTCTGGGAGCCAGCCATGCTGCA 264  
QY 40 sLeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGlnGlnGln 60  
DB 265 CCTGCTTCAGAAACAGGCGCTCTCTGAGACCTCCAGCGCTGCTGGAGGAGAAATCAAGA 324  
QY 60 uLeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeu 80  
DB 325 GCTCCGAGATGCATCCGCGCAGAGCAACAGATTTCTGCGGAGCGCTGCGAGGAGCTTC 384  
QY 80 uHisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAl 100
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Qy 259 InLeuGluAspLeuLys 264
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